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(54) New tissue plasminogen activator.

(57) This invention discloses a new tissue plasminogen activator which has strong activity for converting plasminogen into plasmin that degrades the fibrin network of blood clot to form soluble products and therefore is useful as a thrombolytic agent, a DNA sequence encoding amino acid sequence of it, a process for producing it and a pharmaceutical composition comprising it.

EP 0 302 456 A1

NEW TISSUE PLASMINOGEN ACTIVATOR

This invention relates to a new tissue plasminogen activator. More particularly, it relates to a new tissue plasminogen activator which has strong activity for converting plasminogen into plasmin that degrades the fibrin network of blood clot to form soluble products and therefore is useful as a thrombolytic agent, to DNA sequence encoding amino acid sequence of it, to a process for producing it and pharmaceutical composition comprising it.

The whole amino acid sequence and structure of a native human "tissue plasminogen activator" (hereinafter referred to as "t-PA") and DNA sequence coding for it derived from a human melanoma cell (Bowes) have already been clarified by recombinant DNA technology [Cf. Nature 301, 214 (1983)].

However, the native t-PA obtained by expressing DNA encoding amino acid sequence of the native t-PA in E. coli can hardly be refolded and therefore only an extremely small quantity of the active t-PA can be recovered from the cultured cells of the E. coli.

From the results of various investigations, inventors of this invention succeeded in producing new t-PA which is well refolded, even in a form of the resultant product obtained from the E. coli cells to give an active t-PA, and display a longer half-life and has a stronger thrombolytic activity than the native t-PA.

The new t-PA of this invention may be represented by the following amino acid sequence (I) as its primary structure.

```
                        180                                 190
R-GluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHisSer
                        200                                 210
LeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLysVal
                        220                                 230
TyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArg
                        240                                 250
AsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrp
                        260                                 270
GluTyrCysAspValProSerCysSerThrCysGlyLeuArgGln----------Y-----
          277           280                                 290
----------X-GlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIle
                        300                                 310
PheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSer
                        320                                 330
SerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeu
                        340                                 350
ThrValIleLeuGlyArgThrTyrArgValValProGluGluGluGluGlnLysPheGlu
                        360                                 370
ValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAla
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380 390
LeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArgThr
400 410
ValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGly
420 430
TyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisVal
440 450
ArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAsp
460 470
AsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAla
480 490
CysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuVal
500 510
GlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLys
520 527
ValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro

92 100
wherein R is Ser- or CysTyrGluAspGlnGlyIleSerTyrArgGlyThrTrp
110 120
SerThrAlaGluSerGlyAlaGluCysThrAsnTrpAsnSerSerAlaLeuAlaGlnLys
130 140
ProTyrSerGlyArgArgProAspAlaIleArgLeuGlyLeuGlyAsnHisAsnTyrCys
150 160
ArgAsnProAspArgAspSerLysProTrpCysTyrValPheLysAlaGlyLysTyrSer
170 174
SerGluPheCysSerThrProAlaCysSer-

X is -Lys-, -Ile- or bond and

Y is -TyrSerGlnProGlnPheArgIle-, -TyrSerGlnProGlnPheAspIle-, -TyrSerGlnProIleProArgSer- or -ThrLeuArgProArgPheLysIle-.

[The numbering of the amino acid sequences of the t-PA is according to that described in Nature 301, 217 (1983)]

In the above amino acid sequence, Asn^{184}, Asn^{218} and Asn^{448} may be glycosylated depending on the nature of host cellular environment in the process for the preparation thereof by recombinant DNA technology.

In this specification, the following code names are conveniently employed for the new t-PAs of this invention.

TTktPA

In the above amino acid sequence (I), R is Ser-, X is -Lys- and Y is -TyrSerGlnProGlnPheArgIle-.

TTitPA

In the above amino acid sequence (I), R is Ser-, X is -Ile- and Y is -TyrSerGlnProGlnPheArgIle-.

TQitPA

In the above amino acid sequence (I), R is the residues labelled Cys^{92} to Ser^{174}- of the native tPA, X is -Ile- and Y is -TyrSerGlnProGlnPheArgIle-.

TQktPA

In the above amino acid sequence (I), R is the residues labelled Cys^{92} to Ser^{174}- of the native tPA, X is -Lys- and Y is -TyrSerGlnProGlnPheArgIle-.

STTktPA

In the above amino acid sequence (I), R is Ser-, X is -Lys- and Y is -TyrSerGlnProGlnPheAspIle-.

STQktPA

In the above amino acid sequence (I), R is the residues labelled Cys^{92} to Ser^{174}- of the native tPA, X is -Lys- and Y is -TyrSerGlnProGlnPheAspIle-.

STQitPA

In the above amino acid sequence (I), R is the residues labelled Cys^{92} to Ser^{174} of the native tPA, X is -Ile- and Y is -TyrSerGlnProGlnPheAspIle-.

thTTtPA

In the above amino acid sequence (I), R is Ser-, X is bond and Y is -TyrSerGlnProIleProArgSer-

uTTtPA

In the above amino acid sequence (I), R is Ser-, X is -Lys- and Y is -ThrLeuArgProArgPheLysIle-

The native t-PA is a single chain serine protease which is converted to a 2-chain form, heavy and light chains, linked by single disulfide bond with plasmin. The light chain (L) is a protease domain and therefore contains the active-site of the enzyme. The heavy chain (H) has a finger domain (F) (having homology to fibronectin), a growth factor domain (E) (homologous to epidermal growth factor) and two kringles (i.e. kringle 1 and kringle 2 domains; K_1 and K_2) having triple disulfide bonds. Accordingly, the native t-PA is composed of five functional domains F, E, K_1, K_2 and L [Cf. European Patent Application laid open No. 0196920 and Proc. Natl. Acad. Sci. USA 83 4670 (1986)].

Therefore, it is to be understood that this invention also provides

(1) finger and growth factor domains lacking t-PA without glycosylation and

(2) finger and growth factor domains lacking t-PA essentially free from other proteins of human and animal origin.

The above-defined t-PA includes t-PA essentially consisting of kringle 1 and kringle 2 domains of the heavy chain and the light chain of the native t-PA, and a t-PA prepared by deletion or substitution of the amino acid sequence of said t-PA (e.g. t-PA essentially consisting of kringle 2 domain of the heavy chain and the light chain of the native t-PA, the above-exemplified t-PAs in which Lys^{277} is substituted with Ile^{277}, and/or Arg^{275} is substituted with Gly^{275}, Glu^{275}, Asp^{275}, etc.).

The new t-PA of this invention can be prepared by recombinant DNA technology and polypeptide synthesis.

Namely, the new t-PA of this invention can be prepared by culturing a host cell transformed with an expression vector comprising DNA encoding an amino acid sequence of the new t-PA in a nutrient medium, and recovering the new t-PA from the cultured broth.

In the above process, particulars of which are explained in more detail as follows.

The host cell may include a microorganism [bacteria (e.g. Escherichia coli, Bacillus subtilis, etc.), yeast (e.g. Saccharomyces cerevisiae, etc.)], cultured human and animal cells (e.g. CHO cell, L929 cell, etc.) and cultured plant cells. Preferred examples of the microorganism may include bacteria, especially a strain belonging to the genus Escherichia (e.g. E. coli HB 101 ATCC 33694, E. coli HB 101-16 FERM BP-1872, E. coli 294 ATCC 31446, E. coli χ 1776 ATCC 31537, etc.), yeast, animal cell lines(e.g. mouse L929 cell, Chinese hamster ovary(CHO) cell, etc.) and the like.

When the bacterium, especially E. coli is used as a host cell, the expression vector is usually comprising at least promoter-operator region, initiation codon, DNA encoding the amino acid sequence of the new t-PA, termination codon, terminator region and replicatable unit. When yeast or animal cell is used as host cell, the expression vector is preferably composed of at least promoter, initiation codon, DNA encoding the amino acid sequence of the signal peptide and the new t-PA and termination codon and it is possible that enhancer sequence, 5'- and 3'-noncoding region of the native t-PA, splicing junctions, polyadenylation site and replicatable unit are also inserted into the expression vector.

The promoter-operator region comprises promoter, and Shine-Dalgarno (SD) sequence (e.g. AAGG, etc.) Examples of the promoter-operator region may include conventionally employed promoter-operator region (e.g. lactose-operon, PL-promoter, trp-promoter, etc.) and the promoter for the expression of the new t-PA in mammalian cells may include HTLV-promoter, SV40 early or late-promoter, LTR-promoter, mouse metallothionein I(MMT)-promoter and vaccinia-promoter.

Preferred initiation codon may include methionine codon (ATG).

The DNA encoding signal peptide may include the DNA encoding signal peptide of t-PA.

The DNA encoding the amino acid sequence of the signal peptide or the new t-PA can be prepared in a conventional manner such as a partial or whole DNA synthesis using DNA synthesizer and/or treatment of the complete DNA sequence coding for native or mutant t-PA inserted in a suitable vector (e.g. pTPA21, pTPA25, pTPA102, p51H, pN53, pST112, etc.) obtainable from a transformant [e.g. E. coli LE 392λ^+ - (pTPA21), E. coli JA 221 (pTPA 25) ATCC 39808, E. coli JA 221 (pTPA 102) (Lys 277 → Ile) ATCC 39811, E. coli JM109(p51H) FERM P-9774, E. coli JM109(pN53) FERM P-9775, E. coli DH-1(pST112) FERM BP-1966, etc.], or genome in a conventional manner (e.g. digestion with restriction enzyme, dephosphorylation with bacterial alkaline phosphatase, ligation using T4 DNA ligase).

The termination codon(s) may include conventionally employed termination codon (e.g. TAG, TGA, etc.).

The terminator region may contain natural or synthetic terminator (e.g. synthetic fd phage terminator, etc.).

The replicatable unit is a DNA sequence capable of replicating the whole DNA sequence belonging thereto in the host cells and may include natural plasmid, artificially modified plasmid (e.g. DNA fragment prepared from natural plasmid) and synthetic plasmid and preferred examples of the plasmid may include plasmid pBR 322 or artificially modified thereof (DNA fragment obtained from a suitable restriction enzyme treatment of pBR 322) for E. coli, plasmid pRSVneo ATCC 37198, plasmid pSV2dhfr ATCC 37145 plasmid pdBPV-MMTneo ATCC 37224, plasmid pSV2neo ATCC 37149 for mammalian cell.

The enhancer sequence may include the enhancer sequence (72 bp) of SV40.

The polyadenylation site may include the polyadenlation site of SV40.

The splicing junction may include the splicing junction of SV40.

The promoter-operator region, initiation codon, DNA encoding the amino acid sequence of the new t-PA, termination codon(s) and terminator region can consecutively and circularly be linked with an adequate replicatable unit (plasmid) together, if desired using an adequate DNA fragment(s) (e.g. linker, other restriction site, etc.) in a conventional manner (e.g. digestion with restriction enzyme, phosphorylation using

T4 polynucleotide kinase, ligation using T4 DNA-ligase) to give an expression vector. When mammalian cell line is used as a host cell, it is possible that enhancer sequence, promoter, 5'-noncoding region of the cDNA of the native t-PA, initiation codon, DNA encoding amino acid sequences of the signal peptide and the new t-PA, termination codon(s), 3'-noncoding region, splicing junctions and polyadenlation site are consecutively and circularly be linked with an adequate replicatable unit together in the above manner.

The expression vector can be inserted into a host cell. The insertion can be carried out in a conventional manner (e.g. transformation including transfection, microinjection, etc.) to give a transformant including transfectant.

For the production of the new t-PA in the process of this invention, thus obtained transformant comprising the expression vector is cultured in a nutrient medium.

The nutrient medium contains carbon source(s) (e.g. glucose, glycerine, mannitol, fructose, lactose, etc.) and inorganic or organic nitrogen source(s) (e.g. ammonium sulfate, ammonium chloride, hydrolysate of casein, yeast extract, polypeptone, bactotrypton, beef extracts, etc.). If desired, other nutritious sources [e.g. inorganic salts (e.g. sodium or potassium biphosphate, dipotassium hydrogen phosphate, magnesium chloride, magnesium sulfate, calcium chloride), vitamins (e.g. vitamin B1), antibiotics (e.g. ampicillin) etc.] may be added to the medium. For the culture of mammalian cell, Dulbecco's Modified Eagle's Minimum Essential Medium(DMEM) supplemented with fetal calf serum and an antibiotic is often used.

The culture of transformant may generally be carried out at pH 5.5 - 8.5 (preferably pH 7 - 7.5) and 18 - 40°C (preferable 25 - 38°C) for 5 - 50 hours.

When a bacterium such as E. coli is used as a host cell, thus produced new t-PA generally exists in cells of the cultured transformant and the cells are collected by filtration or centrifugation, and cell wall and/or cell membrane thereof are destroyed in a conventional manner (e.g. treatment with super sonic waves and/or lysozyme, etc.) to give debris. From the debris, the new t-PA can be purified and isolated in a conventional manner as generally employed for the purification and isolation of natural or synthetic proteins [e.g. dissolution of protein with an appropriate solvent (e.g. 8M aqueous urea, 6M aqueous guanidium salts, etc.), dialysis, gel filtration, column chromatography, high performance liquid chromatography, etc.]. When the mammalian cell is used as a host cell, the produced new t-PA is generally exist in the culture solution. The culture filtrate (supernatant) is obtained by filtration or centrifugation of the cultured broth. From the culture filtrate, the new t-PA can be purified in a conventional manner as exemplified above.

It may be necessary to obtain the active t-PA from the cell debris of bacteria in the above case. For refolding of thus produced new t-PA, it is preferably employed a dialysis method which comprises, dialyzing a guanidine or urea solution of the new t-PA in the presence of reduced glutathione (GSH) and oxidized glutathione (GSSG) at the same concentration of glutathiones inside and outside of semipermeable membrane at 4 - 40°C for 2 - 60 hours. In this method, the concentration of the glutathiones is preferably more than 2mM and the ratio of reduced glutathione and oxidized glutathione is preferably 10:1. Further, the glutathiones can be replaced with cysteine and cystine in this method. These method can be preferably used for refolding of all the t-PA including native t-PA produced by DNA recombinant technology.

The new t-PA of this invention is useful as a thrombolytic agent for the treatment of vascular diseases (e.g. myocardial infarction, stroke, heart attack, pulmonary embolism, deep vein thrombosis, peripheral arterial occlusion, etc.). The new t-PA of this invention in admixture with pharmaceutically acceptable carriers can be parenterally to mammals including human being in a form of a pharmaceutical composition such as infusion.

The pharmaceutically acceptable carriers may include various organic or inorganic carrier materials conventionally employed in the preparation of pharmaceutical composition comprising a peptide or protein (e.g. serum albumin etc.).

A dosage of the new t-PA of this invention is to be varied depending on various factors such as kind of diseases, weight and/or age of a patient, and further the kind of administration route.

The optimal dosage of the new t-PA of this invention is usually selected from a dose range of 0.1 - 10mg/kg/day by injection or by infusion.

The total daily amount mentioned above may divisionally be given to the patient for several hours.

Mono(or di, or tri)mer (of oligonucleotides) can be prepared by, for examples the Hirose's method [Cf. Tanpakushitsu Kakusan Kohso 25, 255 (1980)] and coupling can be carried out, for examples on cellulose or polystyrene polymer by a phosphotriester method [Cf. Nucleic Acid Research, 9 1691 (1981). Nucleic Acid Research 10, 1755 (1982)].

Brief explanation of the accompanying drawings is as follows.

Figure 1 shows construction and cloning of plasmid pHVBB.

Figure 2 shows construction and cloning of plasmid pCLiPAxtrp.

Figure 3 shows DNA sequence of BglII DNA fragment (1974 bp).

Figure 4 shows construction and cloning of plasmid pCLiPAΔxtrp.
Figure 5 shows construction and cloning of plasmid pTQiPAΔtrp.
Figure 6 shows construction and cloning of plasmid pTA9004.
Figure 7 shows construction and cloning of plamid pTTkPAΔtrp.
Figure 8 shows DNA sequence of EcoRI DNA fragment (472 bp) and
Figure 9 shows construction and cloning of pTTiPAΔtrp.
Figure 10 shows construction and cloning of plasmid pTQkPAΔtrp.
Figure 11 shows construction and cloning of plasmid pMH9003.
Figure 12 shows construction and cloning of plasmid psTTktrp.
Figure 13 shows construction and cloning of plasmid pZY.
Figure 14 shows construction and cloning of plasmid pSTQitrp.
Figure 15 shows construction and cloning of plasmid pSTQktrp.
Figure 16 shows construction and cloning of plasmid pMH9006.
Figure 17 shows construction and cloning of plasmid pthTTtrp.
Figure 18 shows construction and cloning of plasmid pMH9007.
Figure 19 shows construction and cloning of plasmid puTTtrp.
Figure 20 shows construction and cloning of plasmid pST118.
Figure 21 shows cDNA sequence of a native t-PA in pST112.
Figure 22 shows construction and cloning of plasmid pmTQk118
Figure 23 shows construction and cloning of plasmid pmTQk112.
Figure 24 shows construction and cloning of plasmid pHS9006.
Figure 25 shows construction and cloning of plasmid pHS3020.
Figure 26 shows construction and cloning of plasmid pmTTk.
Figure 27 shows construction and cloning of plasmid pMH3025.
Figure 28 shows construction and cloning of plasmid pmSTTk.
Figure 29 shows DNA sequence of coding region in pTTkPAΔtrp.
Figure 30 shows DNA sequence of coding region in pTTiPAΔtrp.
Figure 31 shows DNA sequence of coding region in pTQkPAΔtrp.
Figure 32 shows DNA sequence of coding region in pTQiPAΔtrp.
Figure 33 shows DNA sequence of coding region in pSTTktrp.
Figure 34 shows DNA sequence of coding region in pSTQktrp.
Figure 35 shows DNA sequence of coding region in pSTQitrp
Figure 36 shows DNA sequence of coding region in puTTtrp.
Figure 37 shows DNA sequence of coding region in pthTTtrp.
Figure 38 shows DNA sequence of coding region in pmTQk112.
Figure 39 shows DNA sequence of coding region in pmTTk.
Figure 40 shows DNA sequence of coding region in pmSTTk.

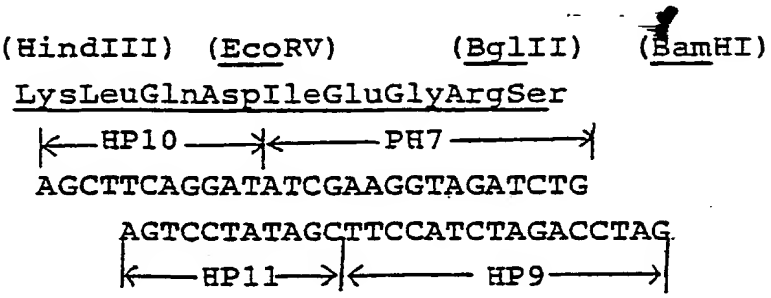
The following Examples are give for the purpose of illustrating this invention, but not limited thereto.

In the Examples, all of the used enzymes (e.g. restriction enzyme, bacterial alkaline phosphatase, T4 DNA ligase) are commercially available and conditions of usage of the enzymes are obvious to the person skilled in the art, for examples, referring to a prescription attached to commercially sold enzymes.

Example 1 (Synthesis of oligonucleotides)

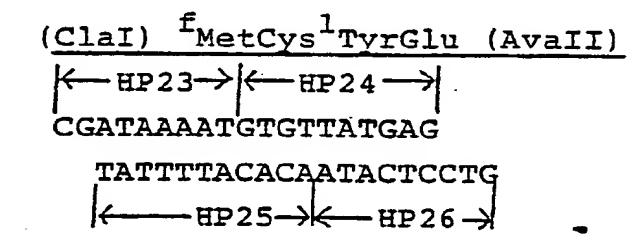
The following oligonucleotides were prepared in a conventional manner described as mentioned above.

1) For pHVBB



HP10; AG-CTT-CAG-GAT
HP7 ; ATC-GAA-GGT-AGA-TCT-G
HP11; C-GAT-ATC-CTG-A
HP9 ; GA-TCC-AGA-TCT-ACC-TT

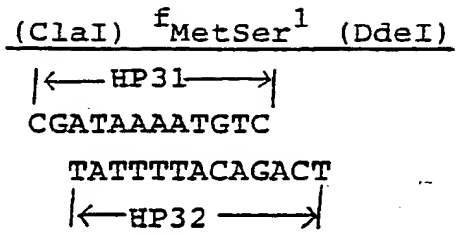
2) For pTQiPAΔtrp and pTQkPAΔtrp



HP23; C-GAT-AAA-AT
HP24; G-TGT-TAT-GAG
HP25; ACA-CAT-TTT-AT
HP26; GTC-CTC-ATA

Cys[1] of TQitPA or TQktPA is corresponding to Cys[32] of the native t-PA reported in Nature 301, 214 (1983).

3) For pTTkPAΔtrp and pTTiPAΔtrp



HP31; C-GAT-AAA-ATG-TC

HP32; TC-AGA-CAT-TTT-AT

Ser[1] of TTktPA or TTitPA is corresponding to Ser[174] of the native t-PA reported in Nature 301, 214 (1983).

Example 2 (Construction and cloning of plasmid pHVBB)
(as illustrated in Fig. 1)

Oligodeoxyribonucleotides HP7 and HP11 (0.2 nmole of each,see: Example 1-(1) were phosphorylated in 20μl of a ligation buffer (1 mM ATP, 50 mM tris-HCl (pH 7.6), 10 mM $MgCl_2$, 20 mM dithiothreitol, 1 mM spermidine, 50 μg/ml bovine serum albumin) with 2.5 units of T4 polynucleotide kinase (Takara Shuzo) at 37°C for 1 hour. After heat inactivation of the enzyme, other oligodeoxyribonucleotides HP10 and HP9 (0.4 nmole of each), 1μl of 20 mM ATP and 900 units of T4 DNA ligase (Takara Shuzo) were added to the reaction mixture. The resultant mixture was incubated at 15°C for 30 minutes to give the crude 27bp DNA fragment.

On the other hand, pCLaHtrp3t (an experssion vector for α-hANP, the preparation of which is described in European Patent Application Laid open No. 0206769) was digested with BamHI and HindIII. The resulting 4137 bp DNA fragment was isolated by 0.8% agarose gel electrophoresis, and ligated to the crude 27 bp DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1 [Cf. Maniatis, T. et al., Molecular cloning p.505 (1982), Cold Spring Harbor Laboratry (New York)]. From one of the ampicillin resistant transformants, the desired plasmid pHVBB (4164bp) was isolated and characterized by restriction endonuclease (BglII, EcoRV, PstI, HindIII and BamHI) digestion.

Example 3 (Construction and cloning of plasmid pCLiPAxtrp)
(as illustrated in Fig. 2)

pHVBB was digested with BglII. The resulting 4164 linear DNA was incubated with bacterial alkaline phosphatase (Takara Shuzo) in 200 mM Tris-HCl (pH 8.0) at 37°C for 1 hour to dephosphorylate the both 5′ ends of the DNA. The resulting DNA was isolated by 5% polyacrylamide gel electrophoresis (PAGE).

On the other hand, pTPA 102 (Lys^{277} → Ile) [an expression vector for a mutant t-PA (Lys^{277} → Ile), a transformant comprising the same, E. coli JA 221 (pTPA 102 (Lys^{277} → Ile) ATCC 39811] was digested with BglII and the 1974bp DNA fragment (DNA sequence of which is shown in Fig. 3) was isolated. The fragment was ligated to the 4164 bp BglII DNA fragment in the presence of T4 DNA ligase. After transformation of E.coli MM294 ATCC 33625, an ampicillin resistant transformant carrying the desired plasmid pCLiPAxtrp (6138 bp), into which the 1974 bp t-PA gene was inserted in a clockwise direction under the down stream of the peptide CLa gene, was obtained. pCLiPAxtrp was characterized by restriction endonuclease (PvuII, EcoRI and BglII) digestion.

Example 4 (Construction and cloning of plasmid pCLiPAΔxtrp)
(as illustrated in Fig. 4)

pCLiPAxtrp was digested with BamHI and SacI and the resultant 5388 bp DNA fragment was isolated. On the other hand, pCLiPAxtrp was digested with Sau3AI and SacI. The resultant 389 bp DNA fragment was ligated to the 5388 bp DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the ampicillin resistant transformants, the desired plasmid pCLiPAΔxtrp (5777 bp) was isolated and was characterized by restriction endonuclease (ClaI, EcoRI, XhoI, NarI and SacI) digestion.

Example 5 (Construction and cloning of plasmid pTQiPAΔtrp)
(as illustrated in Fig. 5)

pTPA102 (Lys^{277} → Ile) as mentioned above was digested with AvaII and BbeI, an isoshizomer of NarI creating 4 nucleotide-long single-stranded cohesive terminal, and the resulting 50 bp DNA fragment encoding Asp^{95} - Ala^{111} of the native t-PA was isolated. On the other hand, the synthetic 19 bp ClaI - AvaII DNA fragment was prepared from HP23, HP24, HP25 and HP26(see:Example 1) using T4 polynucleotide kinase and T4 DNA ligase. It was ligated to the 50 bp DNA fragment with T4 DNA ligase to construct the 69 bp ClaI - BbeI DNA fragment.

pCLiPAΔxtrp was linearlized by BbeI partial digestion. The resultant 5777 bp DNA fragment was digested with ClaI and the 5149 bp DNA fragment was isolated. It was ligated to the 69 bp ClaI - BbeI DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the ampicillin resistant transformants, the desired plasmid pTQiPAΔtrp (5218 bp) was obtained, which was characterized by restriction endonuclease digestion.

E. coli HB101-16 [HB101 ($recA^+$, $supE^+$, htpR16(am), tet^r) FERM P-9502] was transformed with pTQiPAΔtrp to give a transformant, E. coli HB101-16 (pTQiPAΔtrp).

Example 6 (Construction and cloning of plasmid pTA9004)
(as illustrated in Fig. 6)

pCLiPAΔxtrp was digested with DdeI and EcoRI and the 91 bp DNA fragment encoding Glu^{175} Trp^{204} of the native t-PA was isolated. The resultant DNA was ligated to oligodeoxyribonucleotides HP31 and HP32(see:Example 1-(3)) using T4 polynucleotide kinase and T4 DNA ligase. The resultant 103 bpClaI - EcoRI DNA fragment was ligated to the 4397 bp ClaI - EcoRI fragment of pCLiPAΔxtrp in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the ampicillin resistant transformants, the desired plasmid pTA9004 (4500 bp) was obtained.

Example 7 (Construction and cloning of plasmid pTTkPAΔtrp)
(as illustrated in Fig. 7)

pTA9004 was digested with EcoRI and the resultant DNA fragment (4500 bp) was dephosphorylated with bacterial alkaline phosphatase. On the other hand, pTPA21 which comprises the complete cDNA sequence encoding the native t-PA and a portion of the 3'-noncoding region was digested with EcoRI and the 472 bp DNA fragment encoding Asn^{205} - Lys^{361} of the native t-PA (DNA sequence of which is shown in Fig. 8) was isolated. The resultant DNA fragment was ligated to the dephosphorylated 4500 bp EcoRI DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the ampicillin resistant transformants, the desired plasmid pTTkPAΔtrp (4972 bp) was isolated. E. coli HB 101-16 was transformed with pTTkPAΔtrp to give a transformant E. coli HB101-16 (pTTkPAΔtrp).

Example 8 (Construction and cloning of plasmid pTTiPAΔtrp)
(as illustrated in Fig. 9)

pTA9004 was digested with EcoRI and the resultant DNA was dephosphorylated with bacterial alkaline phosphatase. On the other hand, pTPA 102 (Lys^{277} → Ile) as mentioned above was digested with EcoRI

and the 472 bp DNA fragment encoding Asn^{205} - Lys^{361} of the mutant t-PA (Lys^{277} → Ile) was isolated. The resultant DNA fragment was ligated to the dephosphorylated 4500 bp EcoRI DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the ampicillin resistant transformants, the desired plasmid pTTiPAΔtrp (4972 bp) was isolated. E. coli HB101-16 was transformed with pTTiPAΔtrp to give a transformant E. coli HB 101-16 (pTTiPAΔtrp).

Example 9 (Expression and isolation)

A single colony of E. coli HB 101-16 (pTTkPAΔtrp) was inoculated into 5 ml of sterilized L.A broth containing bactotrypton 10 g, yeast extract 5 g, NaCl 5 g, 50μg/ml ampicillin (pH 7.2 - 7.4) in a test tube and incubated at 37°C for 8 hours under shaking condition. The cultured broth was added to 100 ml of sterilized fresh LA broth in a flask and incubated at 37°C for 15 hours under shaking condition. A portion (20 ml) of the resultant broth was added to 400 ml of sterilized M9CA broth containing 25μg/ml ampicillin, and the mixed broth was incubated at 37°C. When A_{600} of the broth reached approximately 0.6, β-indoleacrylic acid was added to the broth in a final concentration of 10μg/ml. The resultant broth was incubated at 37°C for 3 hours, and centrifuged at 4°C, 8, 900 x g for 10 minutes. The harvested cells were suspended in 100 ml of 10 mM Tris-HCl (pH 8.0) containing 5 mM EDTA, and treated with 50 mg of lysozyme at 4°C for 1 hour. The resultant mixture was homogenized by a Biotron blender and centrifuged at 4°C, 8, 900 x g for 30 minutes. The pellets were washed with 100 ml of 50% aqueous glycerol and dissolved in 800 ml of 10 mM Tris-HCl (pH 8.0) containing 8M urea. To the urea solution, 480 mg of GSH (Kojin) and 96 mg of GSSG (Kojin) were added. The resultant mixture was dialyzed twice against 16 liters of a buffer solution (pH 9.5) containing 20 mM acetic acid, 40 mM ammonia, 2 mM GSH and 0.2 mM GSSG at 4°C for 15 hours. After centrifuging the mixture, the supernatant was assayed by the following fibrin plate assay. The fibrin plate assay (FPA) was carried out according to the method [Astrup T. and Müllertz S., Arch. Biochem. Biophys. 40 346 - 351 (1952)] with minor modification. A fibrin plate was prepared by mixing 5 ml of 1.2% human plasminogen-rich fibrinogen (Green - Cross) in 100 mM phosphate buffer (pH 7.2) with 5 ml of thrombin (Mochida, 50 units) in the same buffer, followed by allowing to stand at room temperature for 1 hour. The test solution or human native t-PA (WHO standard) (10 μl of each) were incubated at 37°C for 18 hours. Using the human native t-PA as the standard, the activities of the samples were calculated from the areas of the lysis zones. From the result of assay, the t-PA activity of the supernatant containing TTkPA was 2.3×10^5 IU of the native t-PA/ℓ.

Example 10 (Expression and isolation)

A single colony of E. coli HB 101-16 (pTTiPAΔtrp) was cultured and TTitPA was isolated from the resultant culltured broth in the substantially the same manner as that described in Example 9. The t-PA activity of the resultant supernatant containing TTitPA was 2.0×10^4 IU of the native t-PA/ℓ.

Example 11 (Expression and isolation)

A single colony of E. coli HB 101-16 (pTQiPAΔtrp) was cultured and TQitPA was isolated from the resultant culltured broth in the substantially the same manner as that described in Example 9. The t-PA activity of the resultant supernatant containing TQitPA was 2.0×10^4 IU of the native t-PA/ℓ.

Example 12 (Purification of TTktPA)

All procedures were performed in cold room (at 4 - 6°C). The plasminogen activator, TTktPA in the supernatant renatured was isolated and purified as follows:

In the first step, the supernatant prepared from 20 liter of the cultured broth obtained in a similar manner to that described in Example 9 [TTktPA total activity: 3.4×10^6 IU of the native t-PA (WHO)] was loaded onto benzamidine Sepharose column [1.6 cm x 3 cm : p-aminobenzamidine was linked covalently to CH Sepharose 4B (Pharmacia) by the carbodiimide method described in the literature : Las Holmberg, et al., BBA, 445, 215 - 222 (1976)] equilibrated with 0.05 M Tris-HCl (pH 8.0) containing 1M NaCl and 0.01% (v/v) Tween80 and then washed with the same buffer. The plasminogen activator was eluted with 0.05M

Tris-HCl(pH 8.0) containing 1M arginine and 0.01% (v/v) Tween80.

In the next step, pooled active fractions were applied on IgG coupled Sepharose (FTP 1163) column (1.6 cm x 3 cm) [monoclonal anti t-PA antibody: FTP 1163 (Tsutomu Kaizu et al., Thrombosis Research, 40 91 - 99 (1985) was coupled to CNBr activated Sepharose 4B according to manufacture's instructions] equilibrated with 0.1 M Tris-HCl (pH 8.0). The column was washed with 0.1 M Tris-HCl (pH 8.0) containing 1M NaCl, 0.01% (v/v) Tween80 and Aprotinin (10 KIU/ml, Sigma). Elution was done with 0.1M glycine-HCl (pH 2.5) containing 0.5 M NaCl, 0.01% Tween80 and Aprotinin (10 KIU/ml).

In the last step, pooled active fractions obtained from the IgG Sepharose (FTP1163) column were dialyzed against 1 liter of 0.01 M phosphate buffer (pH 7.4) containing 1.6 M KSCN and 0.01% (v/v) Tween80. The solution dialyzed was concentrated to about 2 ml by dialysis against solid polyethylene glycol 20,000. The concentrate obtained was gel-filtered on a Sephacryl S200HR (Pharmacia, 1.6 cm x 90 cm) in 0.01 M phosphate buffer (pH 7.4) containing 1.6 M KSCN and 0.01% (v/v) Tween80. The pooled active fractions were concentrated to about 10 ml by dialysis against solid polyethylene glycol 20,000 and the concentrate was then dialyzed against 0.1 M ammonium bicarbonate containing 0.15 M NaCl and 0.01% (v/v) Tween80 to give dialyzate containing purified TTktPA (3.4 mg, 7.35 x 10^5 IU of the native t-PA (WHO)-mg•protein).

The TTktPA purified have following characteristics.

(i) Analytical SDS PAGE

A 15% polyacrylamide gel was prepared according to the method of Laemmli (U.K. Laemmli, Nature (London 227, 680 - 685 (1970)). The gel was stained with silver (H.M. Poehling, et al., Electrophoresis, 2, 141 (1981).

TTktPA thus purified migrate on the SDS-PAGE as a single band at 35K Daltons under reducing condition and 32K Daltons under nonreducing condition, whereas material incubated with plasmin Sepharose (Per Wallin, et al., BBA, 719, 318 - 328 (1982)) yielded two bands at 30K Daltons (protease domain) and 13.5K Daltons (kringle domain) in the presence of reducing agent, and only one band at 32K Daltons in the absence of reducing agent.

(ii) HPLC

TTktPA purified was applied to a (4.6 mm x 75 mm) ultrapore RPSC column (Beckman, USA). Elution was performed with a linear gradient of acetonitrile (10 - 60% (v/v) in 0.1% (v/v) trifluoroacetic acid at a flow rate of 1.0 ml/min over 30 minutes.

In this system, TTktPA was eluted as single major species at an acetonitrile concentration of approximately 36.5% (v/v).

(iii) N-terminal sequence analysis

Purified single chain TTktPA was reduced and carboxymethylated, desalted on HPLC (Ultrapore RPSC column, concentrated by Speed Vac Concentrator (Savant) and analyzed using a gas phase sequencer, model 370A (Applied Biosystem). The N-terminal amino acid sequence of thus obtained TTktPA was as follows.

SerGluGlyAsn -

Example 13 (Construction and cloning of plasmid pTQkPAΔtrp)
(as illustrated in Fig. 10)

The plasmid pTQiPAΔtrp was digested with EcoRI. The reaction mixture was dephosphorylated with bacterial alkaline phosphatase and the resultant 4744 bp DNA fragment was isolated. On the other hand, the plasmid pTPA 21 was digested with EcoRI and the resultant 472 bp DNA fragment was isolated. The 472

bp DNA fragment was ligated to the 4744bp DNA fragment in the presence of T4 DNA ligase and the ligation mixture was used to transform E. coli DH-1. From one of the transformants resistant to ampicillin, the desired plasmid pTQkPAΔtrp was isolated and characterized by restriction mapping. E. coli HB101-16 was transformed with the plasmid pTQkPAΔtrp to give a transformant E. coli HB101-16 (pTQkPAΔtrp).

Example 14 (Synthesis of oligonucleotides)

The following oligonucleatides were prepared in a conventional manner described as mentioned above.

1) Linkage sequence for pSTTktrp and pSTQktrp

```
(DdeI)                          (EcoRV)     (StuI)
266          270                275
LeuArgGlnTyrSerGlnProGlnPheAspIleLysGlyGly
|<-------------------  SK1 (40mer)  ---------->|
 TGAGACAGTACAGCCAGCCACAGTTTGATATCAAAGGAGG
   CTGTCATGTCGGTCGGTGTCAAACTATAGTTTCCTCC
|<-----------SK2(37mer)------------------->|
```

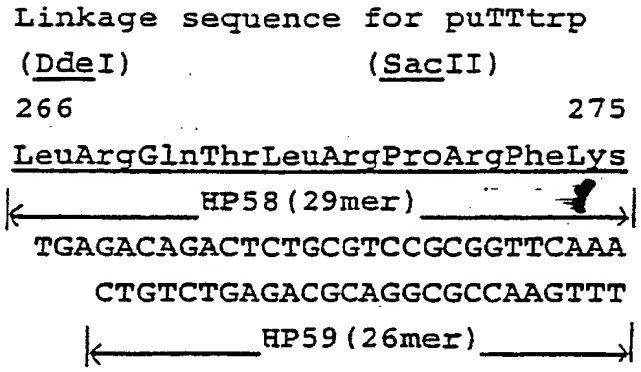
2) Linkage sequence for pSTQitrp

```
(DdeI)                          (EcoRV)     (StuI)
266          270                275
LeuArgGlnTyrSerGlnProGlnPheAspIleIleGlyGly
|<-------------------------HP56(40mer)---------->|
 TGAGACAGTACAGCCAGCCACAGTTTGATATCATAGGAGG
   CTGTCATGTCGGTCGGTGTCAAACTATAGTATCCTCC
|<-----------HP57(37mer)------------------->|
```

3) Linkage sequence for pthTTtrp

```
(DdeI)                        (BglII)   (StuI)
266                             275
LeuArgGlnTyrSerGlnProIleProArgSerGlyGly
|<-------------HP60(37mer)---------------->|
 TGAGACAGTACAGCCAGCCAATTCCTAGATCTGGAGG
   CTGTCATGTCGGTCGGTTAAGGATCTAGACCTCC
|<-----------HP61(34mer)------------------->|
```

4) Linkage sequence for puTTtrp



Numbers above the amino acids refer to the positions of the native t-PA reported by Pennica et al - (Nature 301 214-221, 1983).

Example 15 (Construction and cloning of plasmid pMH9003)
(as illustrated Fig. 11).

The plasmid pTA9004 was digested with EcoRI and StuI, and the resultant 4329 bp DNA fragment was isolated. The DNA fragment was ligated to the synthetic oligodeoxyribonucleotides SK1 and SK2 using T4 polynucleotide kinase and T4 DNA ligase. The reaction mixture was treated with EcoRI to reconstruct the cohesive end digested with EcoRI, and the resultant EcoRI-DdeI DNA fragment (4367 bp) was ligated to the 184 bp EcoRI-DdeI DNA fragment coding Asn^{205} - Leu^{266} of the native t-PA which was obtained from the plasmid pCLiPAΔxtrp in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the transformants resistant to ampicillin, the desired plasmid pMH9003 was isolated and characterized by restriction endonuclease digestion.

Example 16 (Construction and cloning of plasmid pSTTktrp)
(as illustrated in Fig. 12)

The plasmid pMH9003 was digested with StuI and the resulting DNA fragment (4551 bp) was dephosphorylated with calf intestinal phosphatase (Pharmacia AB). On the other hand,the plasmid pCLiPAΔxtrp was digested with StuI and the resultant 419bp DNA fragment coding for Gly^{279} - Ala^{419} of the native t-PA was isolated. The resultant DNA fragment was ligated to the 4551 bp StuI DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the transformants resistant to ampicillin, the desired plasmid pSTTktrp was isolated and characterized by restriction endonuclease digestion. E. coli HB101-16 was transformed with the plasmid pSTTktrp to give a transformant, E. coli HB101-16 (pSTTktrp).

Example 17 (Construction and cloning of plasmid pZY)
(as illustrated in Fig. 13)

The plasmid pTQiPAΔtrp was digested with EcoRI and StuI, and the resultant 4575 bp DNA fragment was isolated. The DNA fragment was ligated to the synthetic oligodeoxyribonucleotides HP56 and HP57 using T4 polynucleotide kinase and T4 DNA ligase. The reaction mixture was treated with EcoRI to reconstruct the cohesive end digested with EcoRI, and the resultant toEcoRI-DdeI DNA fragment (4613bp) was ligated to the 184 bp EcoRI-DdeI DNA coding for Asn^{205} - Leu^{266} of the native t-PA which was prepared from the plasmid pCLiPAΔtrp in the presence of T4 DNA ligase.

The ligation mixture was used to transform E. coli DH-1. From one of the transformants resistant to ampicillin, the desired plasmid pZY was isolated and characterized by restriction mapping.

Example 18 (Construction and cloning of plasmid pSTQitrp)
(as shown in Fig. 14)

The plasmid pZY was digested with StuI and the resulting DNA fragment (4797bp) was dephosphorylated with calf intestinal phosphatase. On the other hand, the plasmid pCLiPAΔxtrp was digested with StuI and the resultant 419 bp DNA fragment coding for Gly^{279} - Ala^{419} of the native t-PA was isolated. The 419 DNA fragment was ligated to the 4797 bp DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1. From one of the transformants resistant to ampicillin, the desired plasmid pSTQitrp was isolated and characterized by restriction mapping. E. coli HB101-16 was transformed with the plasmid pSTQitrp to give a transformant E. coli HB101-16 (pSTQitrp).

Example 19 (Construction and cloning of plasmid pSTQktrp)
(as illustrated in Fig. 15)

The plasmid pSTTktrp was digested with ClaI and EcoRV and the resultant 4656 bp DNA fragment was isolated. On the other hand, the plasmid pSTQitrp was digested with ClaI and EcoRV, and the 560 bp DNA fragment coding for Cys^{1} - Asp^{184} of STQitPA was isolated. The resulting DNA fragment was ligated to the 4656 bp DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1.

From one of the transformants resistant to ampicillin, the desired plasmid pSTQktrp was isolated and characterized by restriction mapping. E. coli HB101-16 was transformed with pSTQktrp to give a transformant HB101-16 (pSTQktrp).

Example 20 (Construction and cloning of plasmid pMH9006)
(as illustrated in Fig. 16)

The plasmid pTA9004 was digested with StuI and EcoRI, and the resultant 4329 bp DNA fragment was isolated. The DNA fragment was ligated to synthetic oligodeoxyribonucleotides HP60 and HP61 using T4 polynucleotide kinase and T4 DNA ligase. The ligation mixture was digested with EcoRI to regenerate the cohesive end digested with EcoRI, and the resultant EcoRI-DdeI DNA fragment (4364bp) was ligated to the 184 bp EcoRI-DdeI DNA fragment coding for Asn^{205} - Leu^{256} of the native t-PA which was prepared from the plasmid pCLiPAΔxtrp. The ligation mixture was based to transform E. coli DH-1. From one of the transformants resistant to ampicillin, the desired plasmid pMH9006 was isolated and characterized by restriction mapping.

Example 21 (Construction and cloning of pthTTtrp)
(as illustrated in Fig. 17)

The plasmid pMH9006 was digested with StuI and the resultant linearized DNA fragment (4548 bp) was dephosphorylated with calf intestinal phosphatase. On the other hand, the plasmid pCLiPAΔxtrp was digested with StuI and the 419 bp DNA fragment encoding Gly^{279} - Ala^{419} of the native t-PA was isolated. The resultant DNA fragment was ligated to the 4548 bp DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1.

From one of the transformants resistant to ampicillin, the desired plasmid pthTTtrp was isolated and characterized by restriction mapping. E. coli HB101-16 was transformed with the plasmid pthTTtrp to give an transformant E. coli HB101-16 (pthTTtrp)

Example 22 (Construction and cloning of plasmid pMH9007)
(as illustrated in Fig. 18)

The plasmid pMH9003 was digested with EcoRI and EcoRV, and the 4340 bp DNA fragment was isolated. The resultant DNA fragment was ligated to the synthetic oligodeoxyribonucleotides HP58 and HP59 by using T4 polynucleotide kinase and T4 DNA ligase. The ligation mixture was treated with EcoRI to regenerate the cohesive terminal digested with EcoRI.

The resultant DNA fragment (4367 bp) was ligated to the 184 bp EcoRI-DdeI DNA fragment obtained from the plasmid pCLiPAΔxtrp in the presence of T4DNA ligase. The ligation mixture was used to transform E. coli DH-1.

From one of the transformants resistant to ampicillin, the desired plasmid pMH9007 was isolated and characterized by restriction mapping.

Example 23 (Construction and cloning of plasmid puTTtrp)
(as illustrated in Fig. 19)

The plasmid pMH9007 was digested with StuI and the resultant linearized DNA fragment (4551 bp) was dephosphorylated with calf intestinal phosphatase. On the other hand, the plasmid pCLiPAΔxtrp was digested with StuI and the resultant 419 bp DNA fragment was isolated. The 419 bp DNA fragment was ligated with the 4551 bp DNA fragment in the presence of T4 DNA ligase. The ligation mixture was used to transform E. coli DH-1.

From one of the transformants resistance to ampicillin, the desired plasmid puTTtrp was isolated and characterized by restriction mapping. E. coli HB101-16 was transformed with the plasmid puTTtrp to give a transformant E. coli HB101-16 (puTTtrp).

Example 24 (Expression and isolation)

E. coli HB101-16 (pTQkPAΔtrp) was cultured and TQktPA was isolated from the resultant cultured broth in substantially the same manner as described in Example 9. The t-PA activity of the resultant supernatant containing TQktPA was 7.7×10^4 IU of the native t-PA/t.

Example 25 (Expression and isolation)

E. coli HB101-16 (pSTTktrp) ,E. coliHB101-16(pSTQktrp), E. coli HB101-16(pSTQitrp), E. coli HB101-16 (pthTTtrp) and E. coli HB101-16 (puTTtrp) were used for the expression of new t-PAs. Cultivation of the bacteria was carried out in substantially the same manner as that described in Example 9. The cell pellets obtained from the resultant cultured broth (200 ml) were suspended in 20 ml of 10 mM phosphate buffered saline (pH 8.0) and sonicated at 4°C for 1 minute. After centrifugation at 15.000 rpm for 20 minutes at 4°C, the resultant pellets were suspended in 20ml of Triton X-100 solution (0.5% Triton X-100, 8% sucrose, 50mM EDTA, 10mM Tris • HCl, pH 8.0) and sonicated at 4°C for 1 minute. The suspension was centrifuged at 15,000 rpm for 20 minute. The resultant pellets were washed with 20 ml of 50 % aqueous glycerol and 20 ml of ice-cold ethanol, successively, and dissolved in 20 ml of 8M urea solution containing 8M urea, 20mM acetic acid, 40mM ammonium hydroxide, 0.4 mM cysteine and 0.04mM cystine, pH9.5) by sonication.

After centrifugation at 15.000 rpm for 20 minutes, the supernatant was diluted to A280 = 0.1 (absorbance at 280nm) with the 8M urea solution. The resultant solution was dialysed against 10 times volume of aqueous solution containing 20 mM acetic acid, 40mM ammonium hydroxide, 0.4mM cysteine and 0.04mM cystine (pH 9.5) at room temperature for hours. In the above procedure, each of the dialysates containing the new t-PAs , STTktPA, STQktPA, STQitPA, thTTtPA or uTTtPA was obatined from the cultured broth of E. coli HB101-16(pSTTktrp), E. coli HB101-16(pSTQktrp), E. coli HB101-16(pSTQitrp), E. coli HB101-16-(pthTTtrp) or E. coli HB101-16(puTTtrp), respectively. Each of the resultant dialysates was subjected to the fibrin plate assay as described in Example 9, respectively. The results are shown in the following table.

New t-PA contained in the dialysate	Activity (IU of the native t-PA/l)
STTktPA	1.1×10^5
STQktPA	2.3×10^4
STQitPA	2.3×10^4
thTTtPA	3.7×10^4
uTTtPA	not detected *)

*)uTTtPA may be a proenzyme like pro-urokinase. Although it was inactive by fibrin plate assay, it was produced in a ratio of 29 µg/l of the cultured broth as analysed by enzyme immunoassay.

Example 26 (Determination of molecular weights of new tPAs)

Molecular weights of the new t-PAs as produced in the above Examples were determined by SDS-PAGE analysis using marker proteins(94,000, 67,000, 45,000, 30,000, 14,400 daltons). The results are shown in the following table.

Molecular weights of the new t-PAs as produced in the above Examples were determined by SDS-PAGE analysis using marker proteins(94,000, 67,000, 45,000, 30,000, 14,400 daltons). The results are shown in the following table.

The new t-PAs	molecular weight(dalton)
TTktPA	approximately 38,000
TTitPA	approximately 38,000
TQitPA	approximately 45,000
TQktPA	approximately 45,000
STTktPA	approximately 38,000
STQktPA	approximately 45,000
STQitPA	approximately 45,000
thTTtPA	approximately 38,000
uTTtPA	approximately 38,000

Example 27 (Identification of DNA sequence)

Expression vectors were characterized and identified by restriction mapping followed by partial DNA sequencing by the dideoxyribonucleotide chain termination method [Smith, A.J.H. Meth. Enzym. 65, 560-580 (1980)] applied to double strand DNA.

The plasmid pTTkPAΔtrp (2µg in 16 µl of 10 mM Tris·HCl (pH 7.4)-1 mM EDTA) was treated with 2MM EDTA (2 µl) and 2N NaOH (2 µl) at room temperature for 5 minutes. To the resultant mixture, 5M ammonium acetate (8 µl) and EtOH (100 µl) was added. The mixture was cooled at -80° C for 30 minutes and centrifuged at 12,000 rpm for 5 minutes. After discarding the supernatant, precipitates were washed with ice-cold 70 % aqueous EtOH and dried in vacuo to give the denatured plasmid.

The plasmid was annealed with a synthetic oligodeoxyribonucleotide primer (5′-ATATTCTGAAAT-GAGCTGT, corresponding to -55--37th position of the tryptophan promoter, 5 ng) in 40 mM Tris·HCl (pH 7.5)-20mM $MgCl_2$ -50mM NaCl at 65° C for 15 minutes followed by gently cooling to room temperature in 30 minutes. The sequencing reaction was performed with T7 polymerase (Sequenase, United States Biochemical Corp) and ^{35}S-dATP (Amersham) according to Tabor, S and Richardson, C.C.,Proc. Natl. Acad. Sci. U.S.A. 84, 4767 - 4771 (1987). The determined sequence (approximately 150 bases from the primer i.e. 35 bases in the tryptophan promoter and 115 bases in the N-terminal coding sequence of TTktPA) was identical with that as expected.

The DNA sequence of pTQkPAΔtrp was performed in a similar manner as described above.

The DNA sequences of pSTTkPAtrp, pthTTtrp and puTTtrp were performed in a similar manner as above except for using a synthetic oligodeoxyribonucleotide (5′-CTCCGGGCGACCTCCTGTG, complementary to the DNA sequence for His^{297} -Gly^{302} of native tPA).

Example 28 (Identification of amino acid sequence)

Purified STTktPA which was purified from the dialysate comprising STTktPA obtained in Example 25 by the similar purification method described in Example 12, was dissolved in 8M urea-50mM Tris•Hcl (pH 8.0)-1.5 % β-mercaptoethanol, and treated with monoiodoacetic acid for carboxymethylation of SH group in Cys residues. The resultant carboxymethylated STTktPA was purified by preparative HPLC using COSMOSIL $5C_4$-300 (4.6 mmø x 50 mm, Nakarai Tesque), and sequenced by a gas-phase sequencer 470A (Applied Biosystems Inc). The N-terminal sequence of the sample was Ser-Glu-Gly-Asn-Ser-Asp-Cys-Tyr-Phe-Gly-Asn-Gly-Ser-Ala-Tyr which was identical with the sequence as expected.

Example 29 (Construction and cloning of pST118)
(as illustrated in Fig. 20)

The plasmid pST112 [an expression vector for a native t-PA which can be isolated from a transformant comprising the same, E. coli DH-1 FERM BP-1966, the complete cDNA sequence of a native t-PA in pST 112 is illustrated in Fig. 21] was digested with BamHI and SalI.

The large DNA was isolated and blunted with DNA polymerase I (Klenow fragment). The resultant DNA fragment was self-ligated with T4 DNA ligase. The ligation mixture was used to transform E. coli HB101. From one of ampicillin resistant transformants, the objective plasmid pST118 was obtained and characterized by restriction mapping.

Example 30 (Construction and cloning of pmTQk112)
(as illustrated in Fig.22 and 23)

The plasmid pST118 was digested with BglII and BbeI. The large DNA fragment was isolated and ligated to synthetic BglII-AvaII DNAs (5′-GATCTTGCTACGAG and 5′-GTCCTCGTAGCAA, each oligomer was phosphorylated with T4 polynucleatide kinase (Takara Suzo)) coding for Arg^{-1} Ser^{1} Cys^{92} Tyr Glu, and Ava II-BbeI DNA coding for Asp^{35} - Gly^{110} of the native tPA from pST118 with T4 DNA ligase (Takara Suzo).

The ligation mixture was used to transform E.coli DH-1. From one of the ampicillin resistant transformants, the objective plasmid pmTQk118 was isolated and characterized by restriction mapping.

On the other hand, the plasmid pST112 was digested with BglII and XmaI. The large DNA fragment was isolated and ligated to 1253 bp BglII-XmaI DNA coding for Arg^{-1} - Val^{507} from pmTQk118 with T4 DNA ligase to give pmTQk112, an expression vector for mTQktPA in mammalian cell.

Example 31 (Construction and cloning of pmTTk)
(as illustrated in Fig. 24, 25 and 26)

pTTkPAΔtrp was digested with ClaI and EcoRI completely. The large DNA fragment was isolated and ligated to ClaI-DdeI synthetic DNAs (5′-CGATAAAATGGGTCCTAGATC and 5′-TCAGATCTAGGACCCATT-TTAT, each DNA was phosphorylated with T4 polynuclectide kinase) including BglII restriction site and 91bp DdeI-EcoRI DNA coding for Glu^{175}-Trp^{204} from pTTkPAΔtrp with T4 DNA ligase to give pHS9006. pTTkPAΔtrp was digested with EcoRI (partial) and ApaI. The 781bp DNA fragment was isolated and ligated to 4.1 kbp EcoRI-ApaI DNA fragment from pHS9006 to give pHS3020 coding for Arg^{-1} plus Ser^{174} - Pro^{527}.

pHS3020 was digested with BglII and SmaI. The small DNA fragment coding for Arg^{-1} plus Ser^{174}-Pro^{508} was isolated and ligated to the BglII-SmaI large DNA fragment from pmTQk112 to give pmTTk, an expression vector for TTktPA in mammalian cell.

Example 32 (Construction and cloning of pmSTTk)
(as illustrated in Fig.27 and 28)

pHS9006 was digested with EcoRI. The large DNA fragment was isolated, dephosphorylated with calf intestinal phosphatase (Pharmacia) and ligated to the 472bp EcoRI DNA coding for Asn^{205} - Asp^{275} - Lys^{36}: from pSTTkΔtrp to give pMH3025. pMH3025 was digested with BglII and SmaI. The small DNA fragment was isolated and ligated to the large fragment BglII-SmaI DNA from pmTQk112 to give pmSTTk, an expression vector for STTktPA in mammalian cell.

Example 33 (Expression)

Construction of L-929 Transformants

A. Preparation of the Cells

A culture of L-929 cell line was used in this example. L-929 cells can be generated from ATCC #CCL-1, and were maintained in DMEM containing kanamycin and 10% (vol/vol) fetal calf serum at 37° C in 5% CO_2. These cells were plated in a cell density of 5 x 10^5 per 10 cm petri dish on the day before transformation, and provided 50-60% confluency on the day transformation. The media was changed three hours before the transformation. Two 10 cm petri dishes of cells were used to each transformation.

B. Preparation of the DNA solution

Plasmid DNA was introduced into L-929 cells using a calcium phosphate technique in a similar manner to that described in Gorman, DNA Cloning II, 143 (1985), IRL press.

Thirty μg of the expression plasmid (pmTQk112, pmTTk or pmSTTk) plus 3μg of plasmid pSV2neo ATCC No. 37149 was added to 186 μl of 2 M $CaCl_2$ and 1.3 ml of water. 1.5 ml of the DNA solution was then added dropwise to 1.5 ml of 2 x HBS (1.63% NaCl, 1.19% Hepes, 0.04% Na_2HPO_4 pH 7.12) under bubbling. The mixture was allowed to stand 30 minutes at room temperature before it was added to the cells.

C. Transfection of the cells

The 0.6 ml of the DNA solution was added to a 10 cm petri dish of L-929 cells with gentle agitation and incubated at 37° C for 18 hours in a CO_2 incubator. The cells were washed twice with DMEM. Complete fresh growth media containing 10% FCS was then added, and the cells were incubated at 37° C for 24 hours in a CO_2 incubator. The cells were trypsinized and subcultured 1:10 into selective medium composed of DMEM containing 300 μg/ml geneticin (G418) and 10% FCS.

Cells which express the phosphotransferase (neo^r gene product) can survive in the selective media and form colonies. Medium was changed every 3-4 days and colonies were isolated after 12-14 days. G418 resistant colonies were picked up by mild trypsinization in small cylinders, grown to mass cultures and tested for the secretion of mutant t-PA. The cells were grown in 1.7 cm diameter muti-well plate dishes with 3 ml of the medium to a total of about 3 x 10^5 cells. Medium was removed and washed with PBS. Cells were cultured in 1 ml of inducible culture media composed of DMEM containing 0.04 mM $ZnSO_4$, 1mM sodium butylate and 2% FCS at 37° C for 24 hours and activity of mutant t-PA in the medium was confirmed an indirect spectrophotometric assay using the chromogenic agent S2251 [Cf. Thrombosis Research 31, 427 (1983)].

E. coli DH-1 was transformed with the plasmid, pmTQk112, pmTTk or pmSTTk for the purpose of the deposit in a conventional manner.

The following microorganisms shown in the above Examples have been desposited with one of the

INTERNATIONAL DEPOSITORY AUTHORITY ON THE BUDAPEST TREATY. Fermentation Research Institute, Agency of Industrial Science and Technology residing at 1-3, Higashi 1 chome, Tsukuba-shi, Ibaraki-ken305, Japan since July 30, October 13 and November 5, 1987 and July , 1988 ,and were assigned the following deposit numbers, respectively.

Microorganisms	Deposit number
Escherichia coli HB101-16	FERM BP-1872
Escherichia coli HB101-16 (pTTkPAΔtrp)	FERM BP-1871
Escherichia coli HB101-16 (pTTiPAΔtrp)	FERM BP-1869
Escherichia coli HB101-16 (pTQiPAΔtrp)	FERM BP-1870
Escherichia coli HB101-16 (pTQkPAΔtrp)	FERM BP-1521
Escherichia coli HB101-16 (pSTTktrp)	FERM BP-1517
Escherichia coli HB101-16 (pSTQitrp)	FERM BP-1516
Escherichia coli HB101-16 (pSTQktrp)	FERM BP-1518
Escherichia coli HB101-16 (pthTTtrp)	FERM BP-1562
Escherichia coli HB101-16 (puTTtrp)	FERM BP-1519
Escherichia coli DH-1(pST112)	FERM BP-1966
Escherichia coli DH-1(pmTQk112)	FERM BP-1965
Escherichia coli DH-1(pmTTk)	FERM BP-1967
Escherichia coli DH-1(pmSTTk)	FERM BP-1964

Claims

1. A tissue plasminogen activator represented by the following amino acid sequence (I) as its primary structure:

```
                    180                                 190
R-GluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHisSer
                    200                                 210
LeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLysVal
                    220                                 230
TyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArg
                    240                                 250
AsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrp
                    260                                 270
GluTyrCysAspValProSerCysSerThrCysGlyLeuArgGln----------Y------
          277       280                                 290
----------X-GlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIle
                    300                                 310
PheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSer
                    320                                 330
SerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeu
                    340                                 350
ThrValIleLeuGlyArgThrTyrArgValValProGluGluGluGlnLysPheGlu
                    360                                 370
ValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAla
                    380                                 390
LeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArgThr
                    400                                 410
ValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGly
                    420                                 430
TyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisVal
                    440                                 450
ArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAsp
```

460 470
AsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAla
480 490
CysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuVal
500 510
GlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLys
520 527
ValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro

92 100
wherein R is Ser- or CysTyrGluAspGlnGlyIleSerTyrArgGlyThrTrp
110 120
SerThrAlaGluSerGlyAlaGluCysThrAsnTrpAsnSerSerAlaLeuAlaGlnLys
130 140
ProTyrSerGlyArgArgProAspAlaIleArgLeuGlyLeuGlyAsnHisAsnTyrCys
150 160
ArgAsnProAspArgAspSerLysProTrpCysTyrValPheLysAlaGlyLysTyrSer
170 174
SerGluPheCysSerThrProAlaCysSer-

X is -Lys-, -Ile- or bond and

Y is -TyrSerGlnProGlnPheArgIle-, -TyrSerGlnProGlnPheAspIle-, -TyrSerGlnProIleProArgSer- or -ThrLeuArgProArgPheLysIle-, and

in the above amino acid sequence, Asn^{184}, Asn^{218} and Asn^{448} may be glycosylated.

2. The tissue plasminogen activator of claim 1, which is not glycosylated.

3. The tissue plasminogen activator of claim 1, in which R is Ser-, X is -Lys- and Y is -TyrSerGlnProGlnPheAspIle-.

4. The tissue plasminogen activator of claim 2, in which R is Ser-, X is -Lys- and Y is -TyrSerGlnProGlnPheAspIle-.

5. A DNA encoding amino acid sequence (I) as defined in claim 1.

6. A recombinant vector comprising DNA encoding amino acid sequence (I) as defined in claim 1.

7. A transformant comprising expression vector of DNA sequence encoding amino acid sequence (I) as defined in claim 1.

8. A process for the production of tissue plasminogen activator fo claim 1 which comprises, culturing a host cell transformed with an expression vector comprising DNA encoding an amino acid sequence (I) as defined in claim 1 in a nutrient medium, and recovering the resultant t-PA from the cultured broth.

9. A pharmaceutical composition comprising tissue plasminogen activator of claim 1 and pharmaceutically acceptable carrier(s).

10. A finger and growth factor domains lacking tissue plasminogen activator essentially free from other proteins of human and animal origin.

11. A finger and growth factor domains lacking tissue plasiminogen activator without glycosylation.

12. A tissue plasminogen activator, essentially consisting of kringle 2 domain of the heavy chain and the light chain corresponding to those of native human tissue plasminogen activator and essentially free of other proteins of human and animal origin.

13. A tissue plasminogen activator, essentially consisting of kringle 2 domain of the heavy chain and the light chain corresponding to those of native human tissue plasminogen activator without glycosylation.

14. The tissue plasminogen activator of claim 13, in which arginine residue at 275 position of the native human tissue plasminogen acitivator is replaced by aspartic acid residue.

Fig. 1 Construction and cloning of plasmid pHVBB

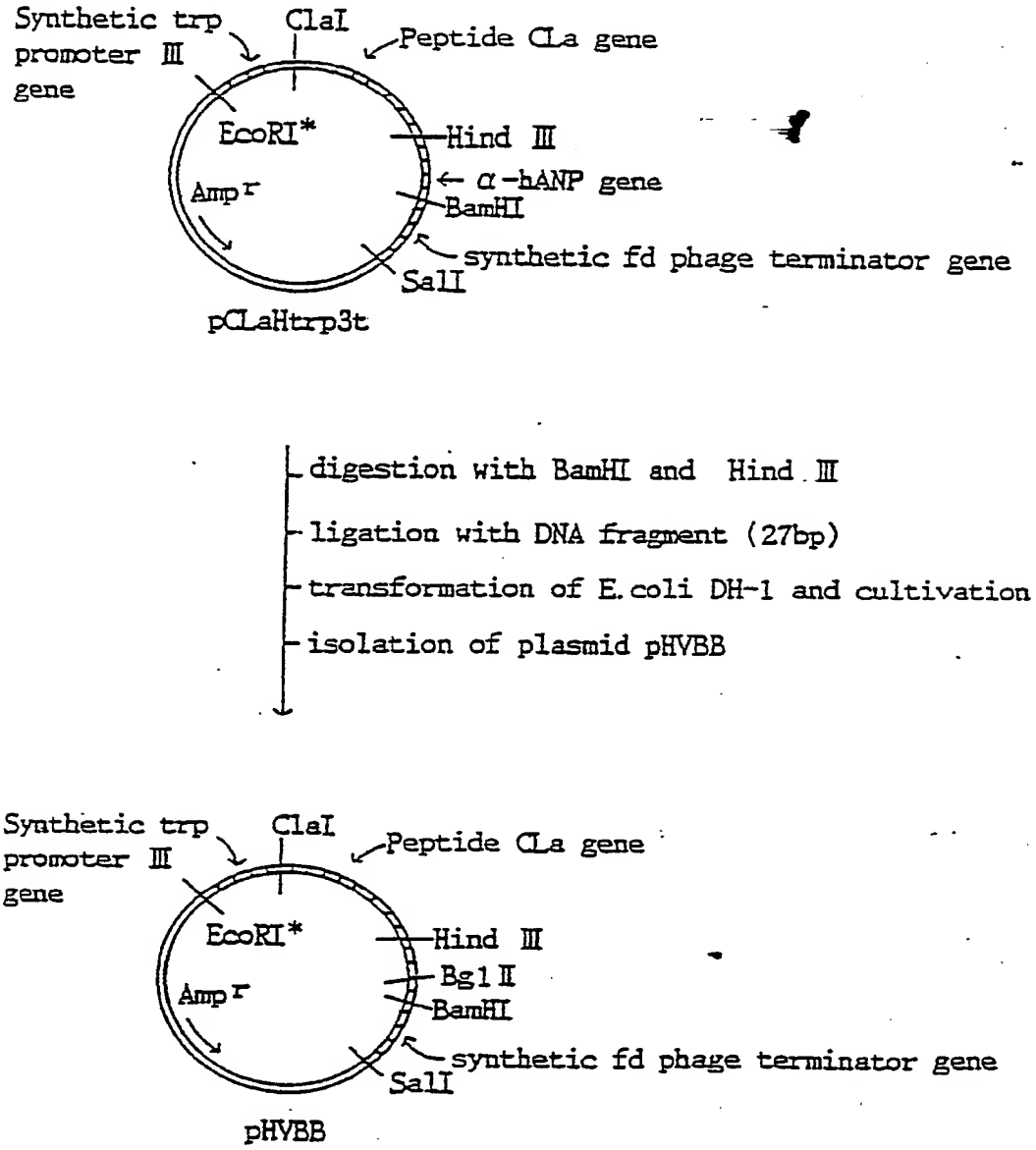


Fig. 2 Construction and cloning of plasmid pCLiPAxtrp

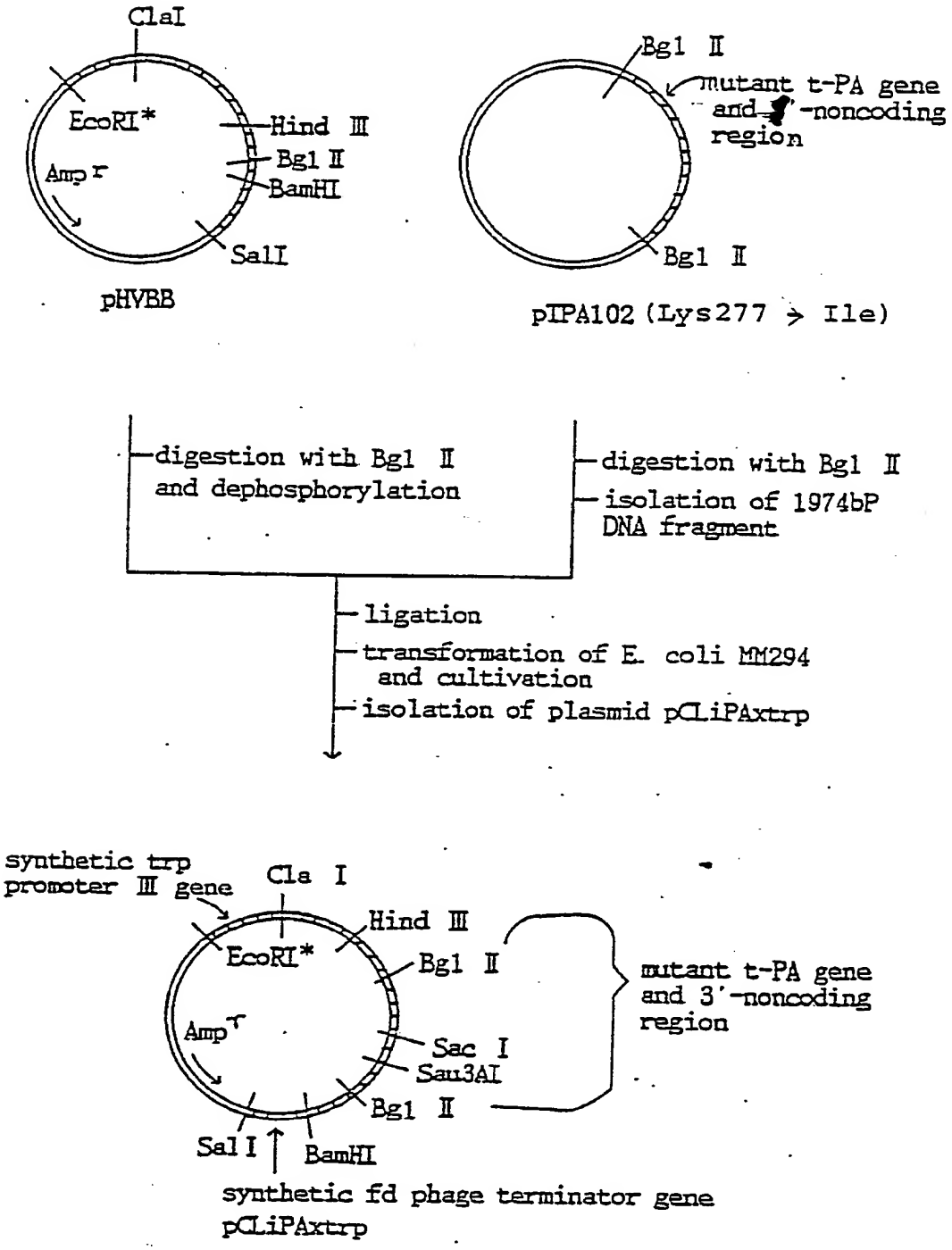


Fig.3-(1)DNA sequence of Bgl II DNA fragment(1974bp)

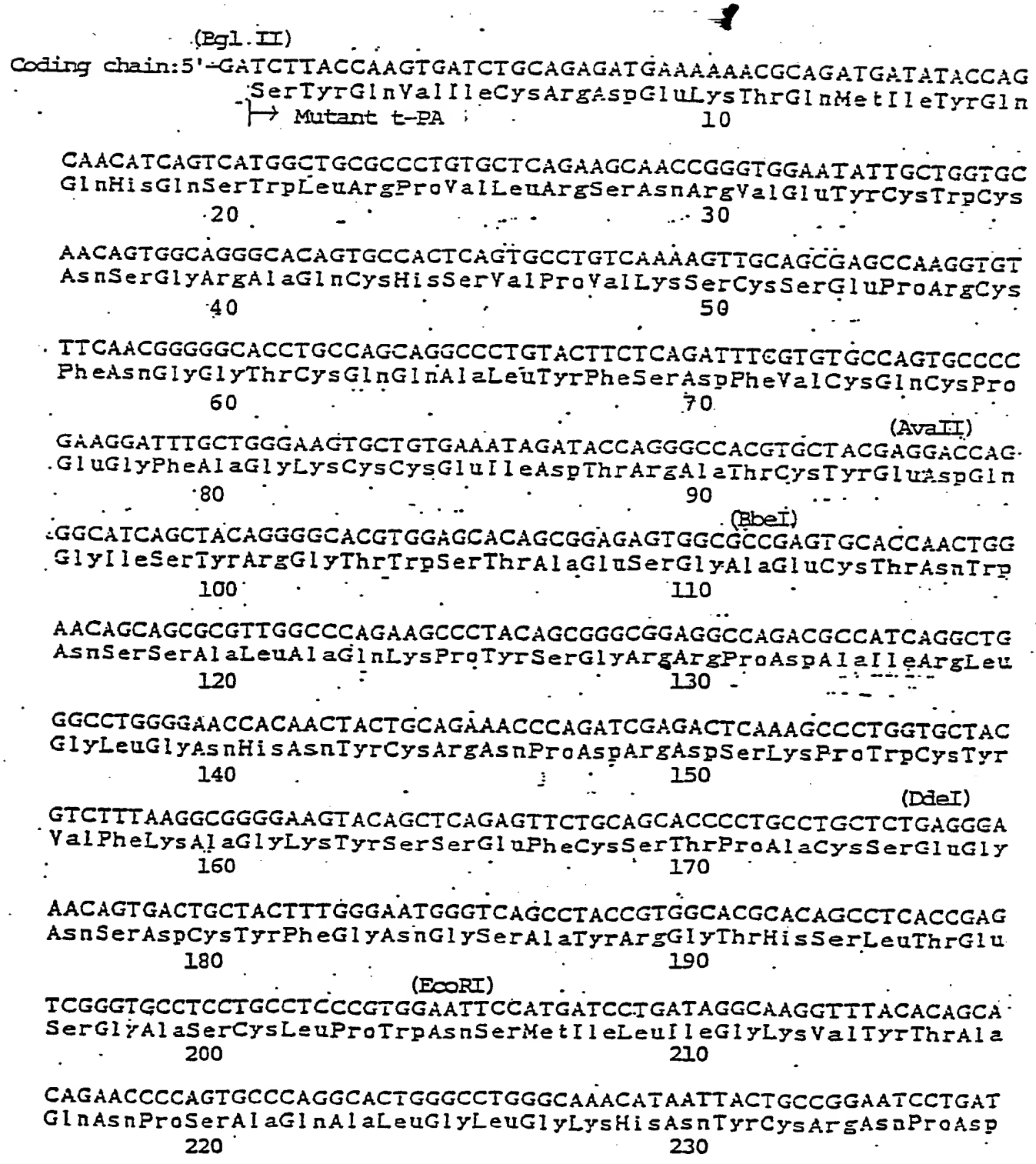


Fig. 3-(2)

```
GGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTACTGT
GlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrpGluTyrCys
          240                                   250

GATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATC
AspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnProGlnPheArgIle
          260                                   270

ATAGGAGGCCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCTTTGCCAAG
IleGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIlePheAlaLys
          280                                   290

CACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATCAGCTCCTGCTGG
HisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSerSerCysTrp
          300                                   310

ATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCACCTGACGGTGATC
IleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeuThrValIle
          320                                   330

TTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA
LeuGlyArgThrTyrArgValValProGlyGluGluGluGlnLysPheGluValGluLys
          340                                   350

                (EcoRI)
TACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCGCTGCTGCAG
TyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAlaLeuLeuGln
          360                                   370

CTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACTGTGTGCCTT
LeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArgThrValCysLeu
          380                                   390

                                        (SacI)
CCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAG
ProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGlyTyrGlyLys
          400                                   410

CATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTAC
HisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisValArgLeuTyr
          420                                   430

CCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTG
ProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAspAsnMetLeu
          440                                   450

TGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTGCACGACGCCTGCCAGGGC
CysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAlaCysGlnGly
          460                                   470

GATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATC
AspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuValGlyIleIle
          480                                   490
```

Fig. 3-(3)

AGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAGGTTACCAAC
SerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLysValThrAsn
500 510

TACCTAGACTGGATTCGTGACAACATGCGACCGTGACCAGGAACACCCGACTCCTCAAAA
TyrLeuAspTrpIleArgAspAsnMetArgPro***⟶ Noncoding
520

(Sau3AI)
GCAAATGAGATCCCGCCTCTTCTTCTTCAGAAGACACTGCAAAGGCGCAGTGCTTCTCTA

CAGACTTCTCCAGACCCACCACACCGCAGAAGCGGGACGAGACCCTACAGGAGAGGGAAG

AGTGCATTTTCCCAGATACTTCCCATTTTGGAAGTTTTCAGGACTTGGTCTGATTTCAGG

ATACTCTGTCAGATGGGAAGACATGAATGCACACTAGCCTCTCCAGGAATGCCTCCTCCC

TGGGCAGAAGTGGCCATGCCACCCTGTTTTCGCTAAAGCCCAACCTCCTGACCTGTCACC

GTGAGCAGCTTTGGAAACAGGACCACAAAAATGAAAGCATGTCTCAATAGTAAAAGAAAC

(Bgl II)
AAGA -3'

Fig. 4 Construction and cloning of plasmid pCLiPAΔxtrp

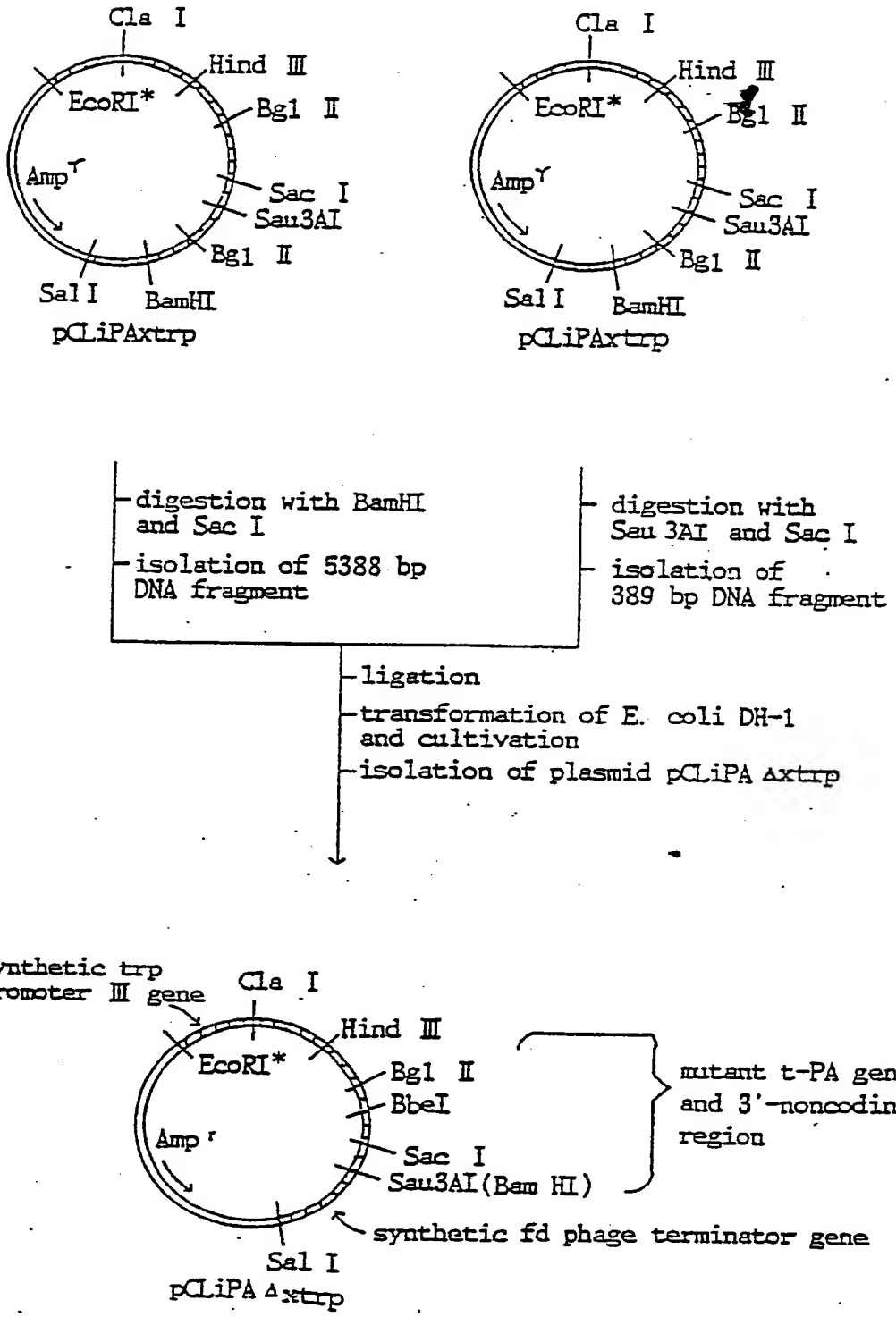
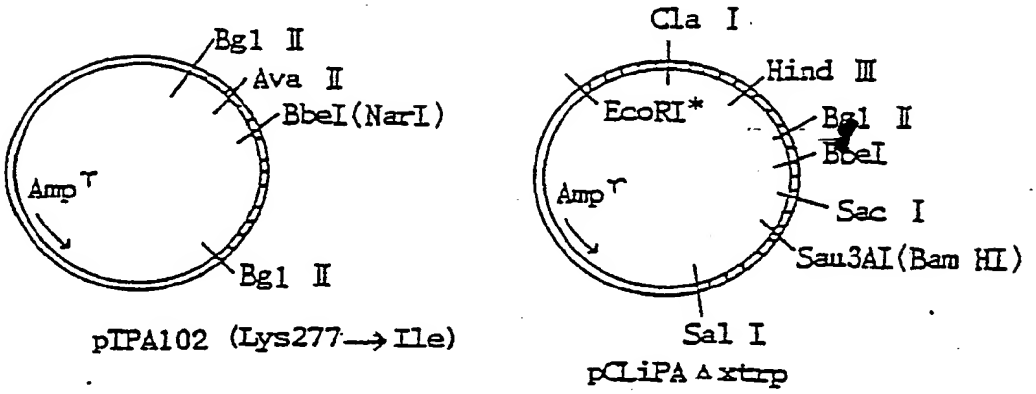
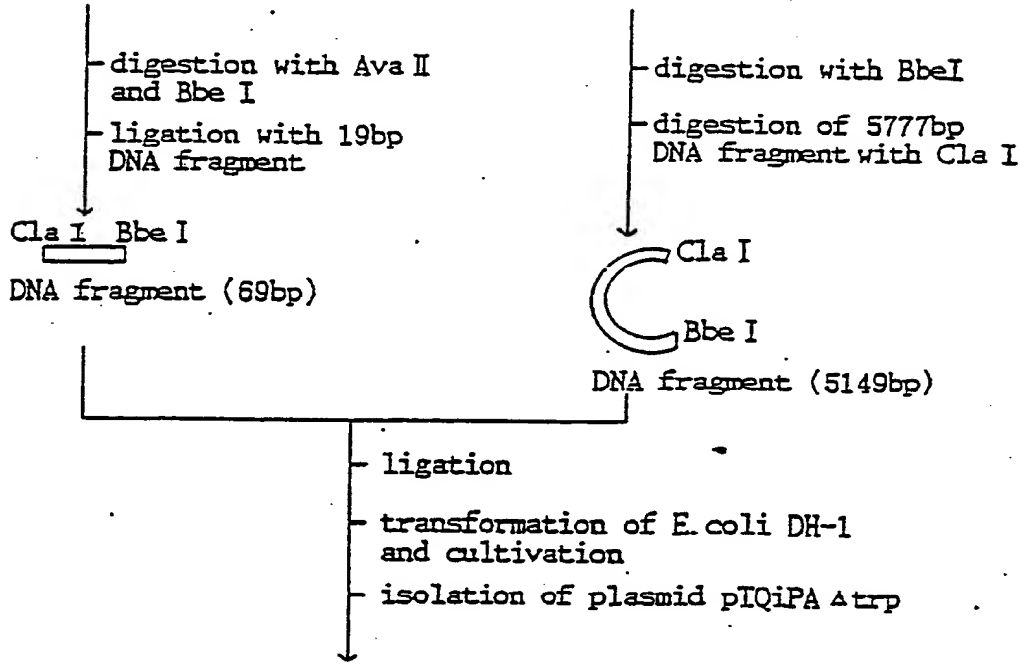


Fig. 5 Construction and cloning of plasmid pIQiPAΔtrp





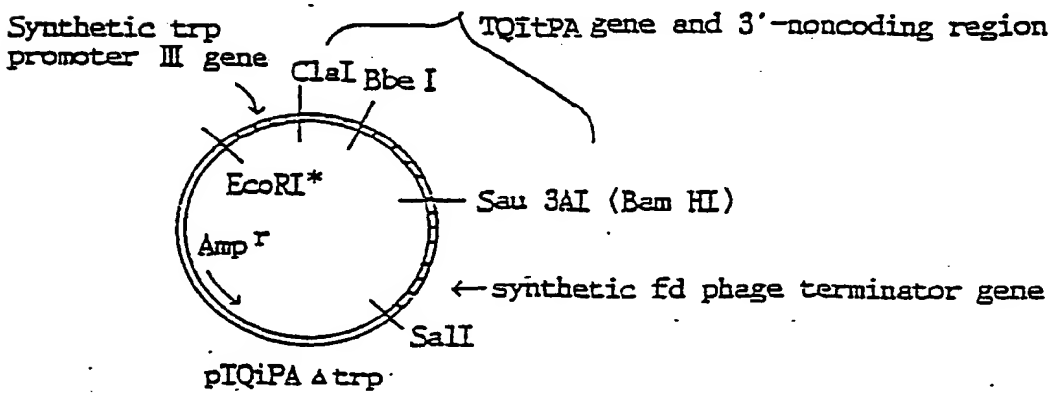
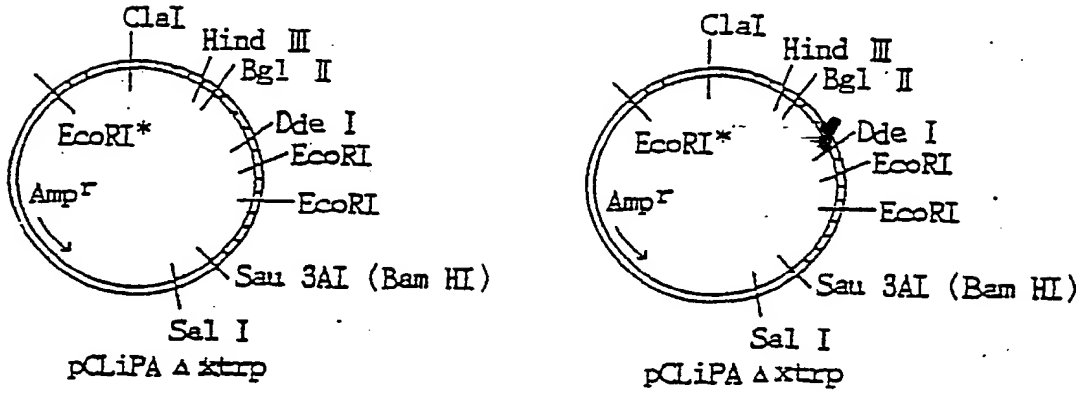
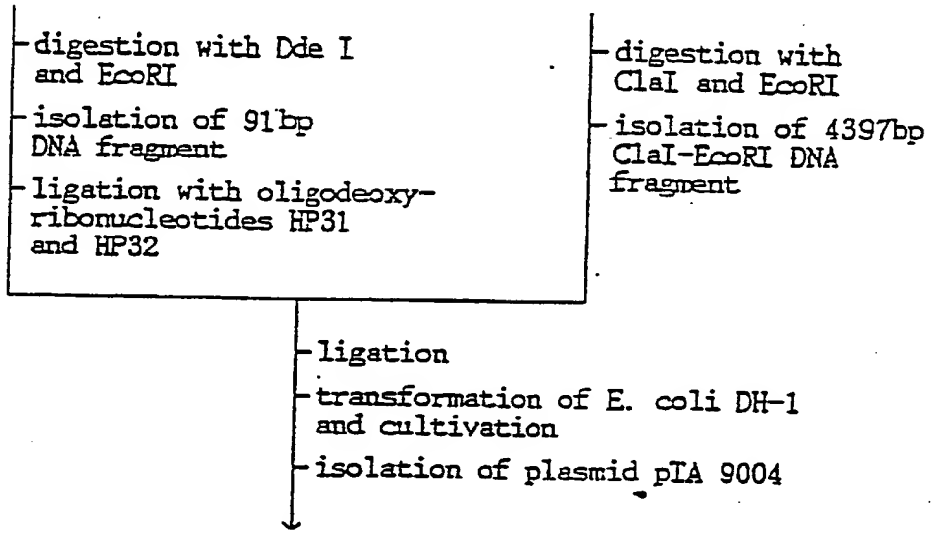


Fig. 6 Construction and cloning of plasmid pTA9004





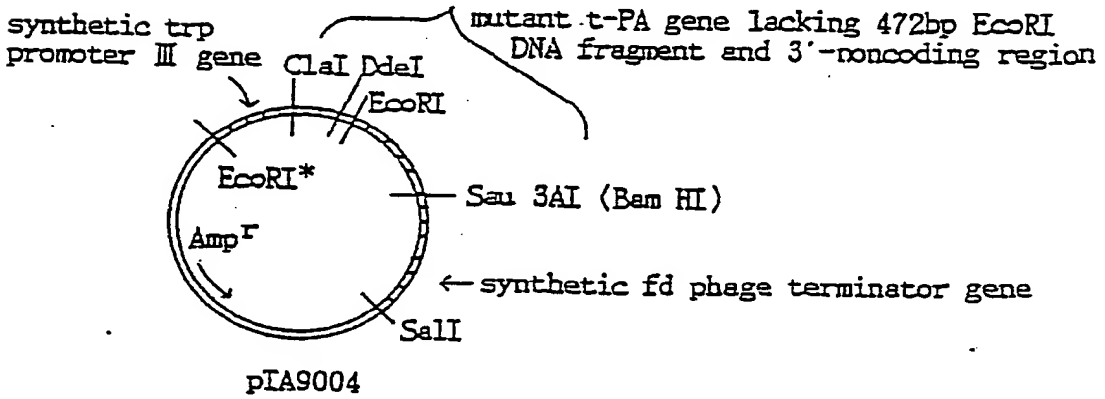


Fig. 7 Construction and cloning of plasmid pTTkPAΔtrp

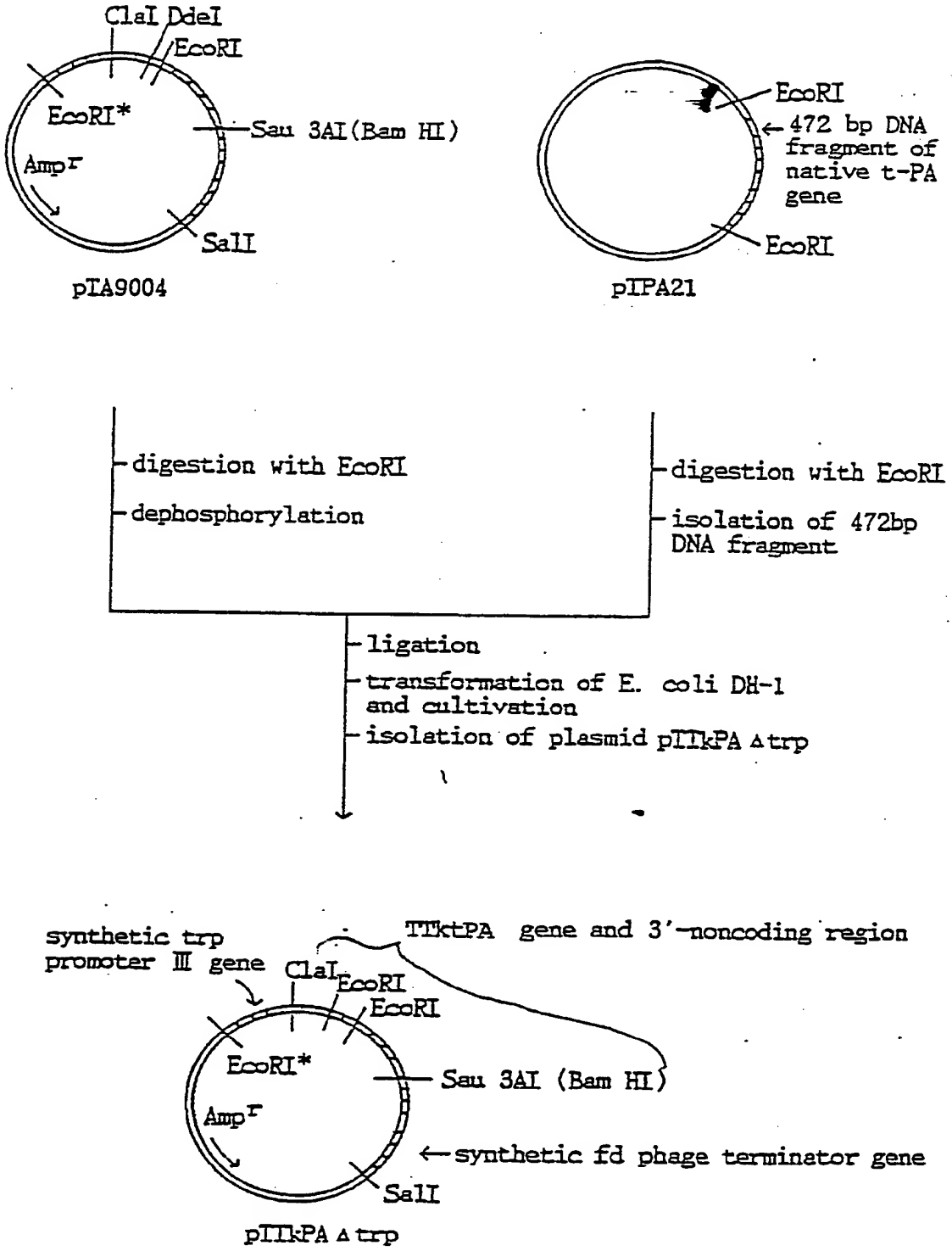


Fig. 8 DNA sequence of EcoRI DNA fragment(472bp)

(EcoRI)

Coding chain: 5'-AATTCCATGATCCTGATAGGCAAGGTTTACACAGCA
Amino acid sequence: AsnSerMetIleLeuIleGlyLysValTyrThrAla

CAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGGAATCCTGAT
GlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArgAsnProAsp

GGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTACTGT
GlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrpGluTyrCys

GATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATC
AspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnProGlnPheArgIle

AAAGGAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCTTTGCCAAG
LysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIlePheAlaLys

CACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATCAGCTCCTGCTGG
HisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSerSerCysTrp

ATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCACCTGACGGTGATC
IleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeuThrValIle

TTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA
LeuGlyArgThrTyrArgValValProGlyGluGluGluGlnLysPheGluValGluLys

(EcoRI)

TACATTGTCCATAAGG -3'
TyrIleValHisLys

Fig. 9 Construction and cloning of plasmid pTTiPAΔtrp

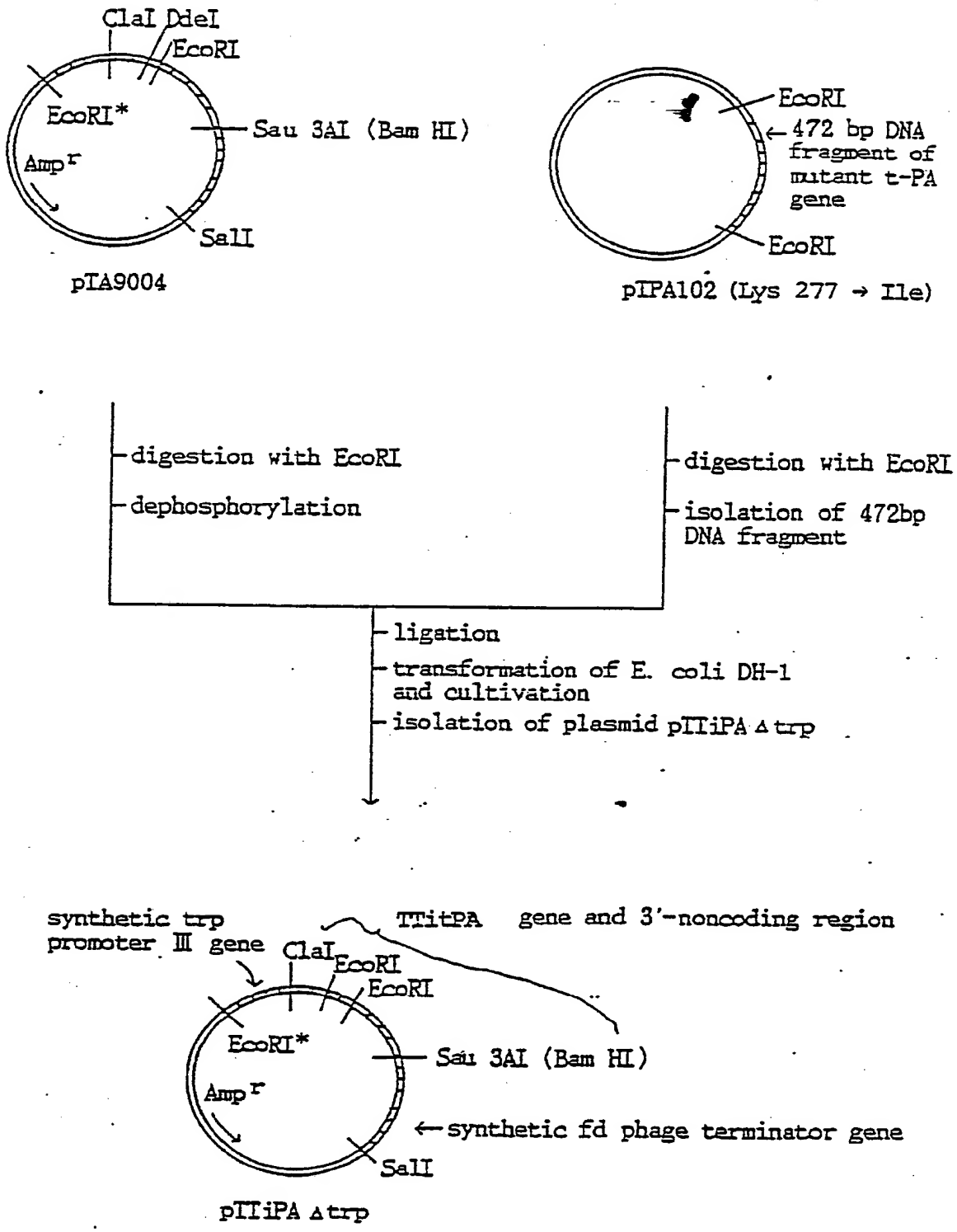


Fig. 10 Construction and cloning of plasmid pIQkPA△trp

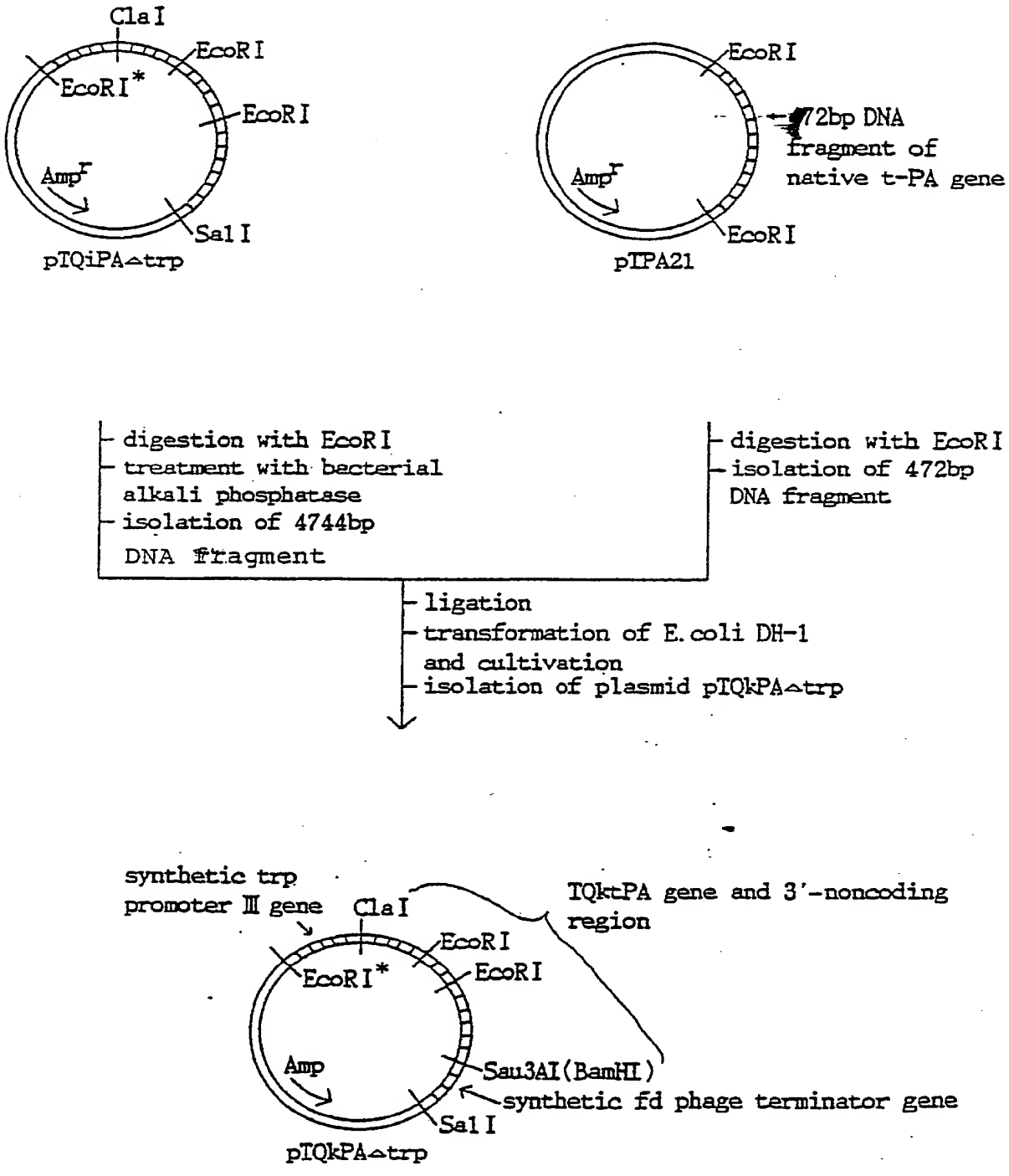


Fig. 11 Construction and cloning of plasmid pMH9003

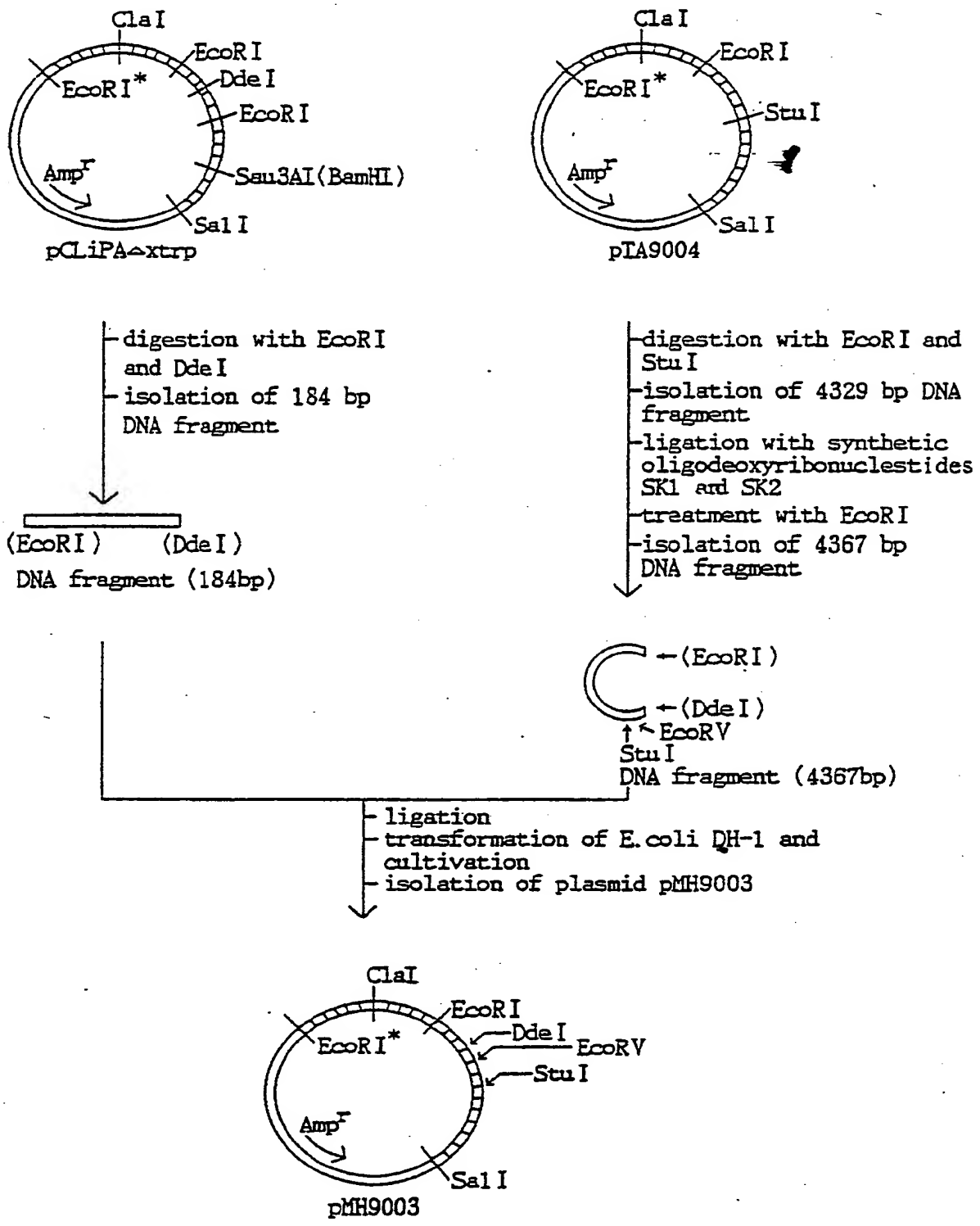
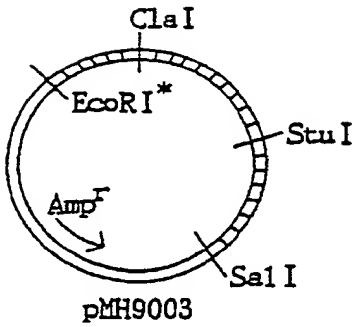
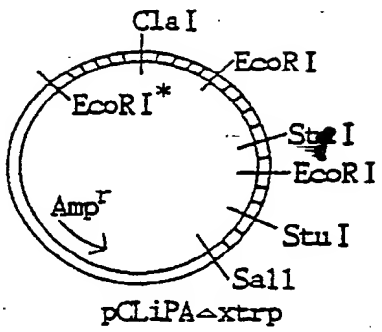
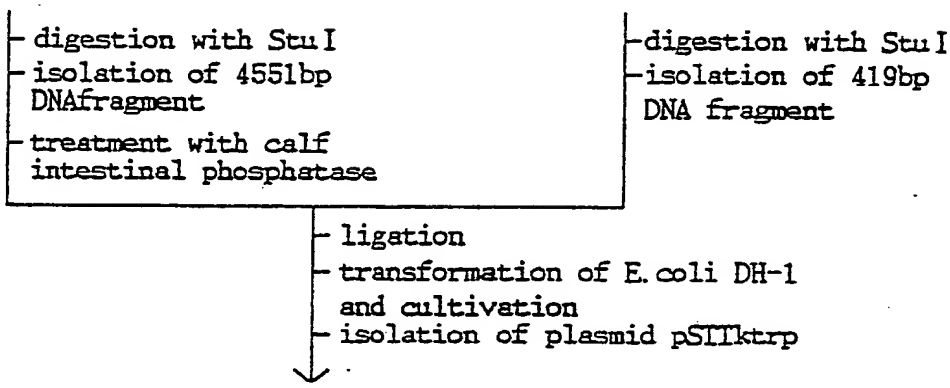


Fig. 12 Construction and cloning of plasmid pSIIktrp







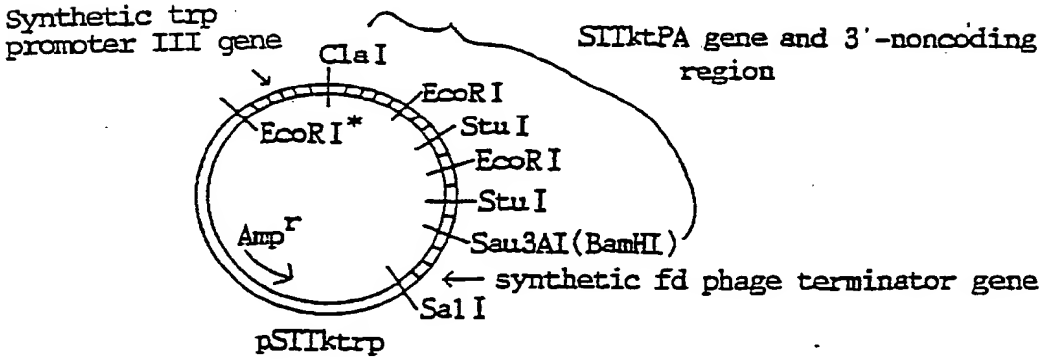


Fig. 13 Construction and cloning of plasmid pZY

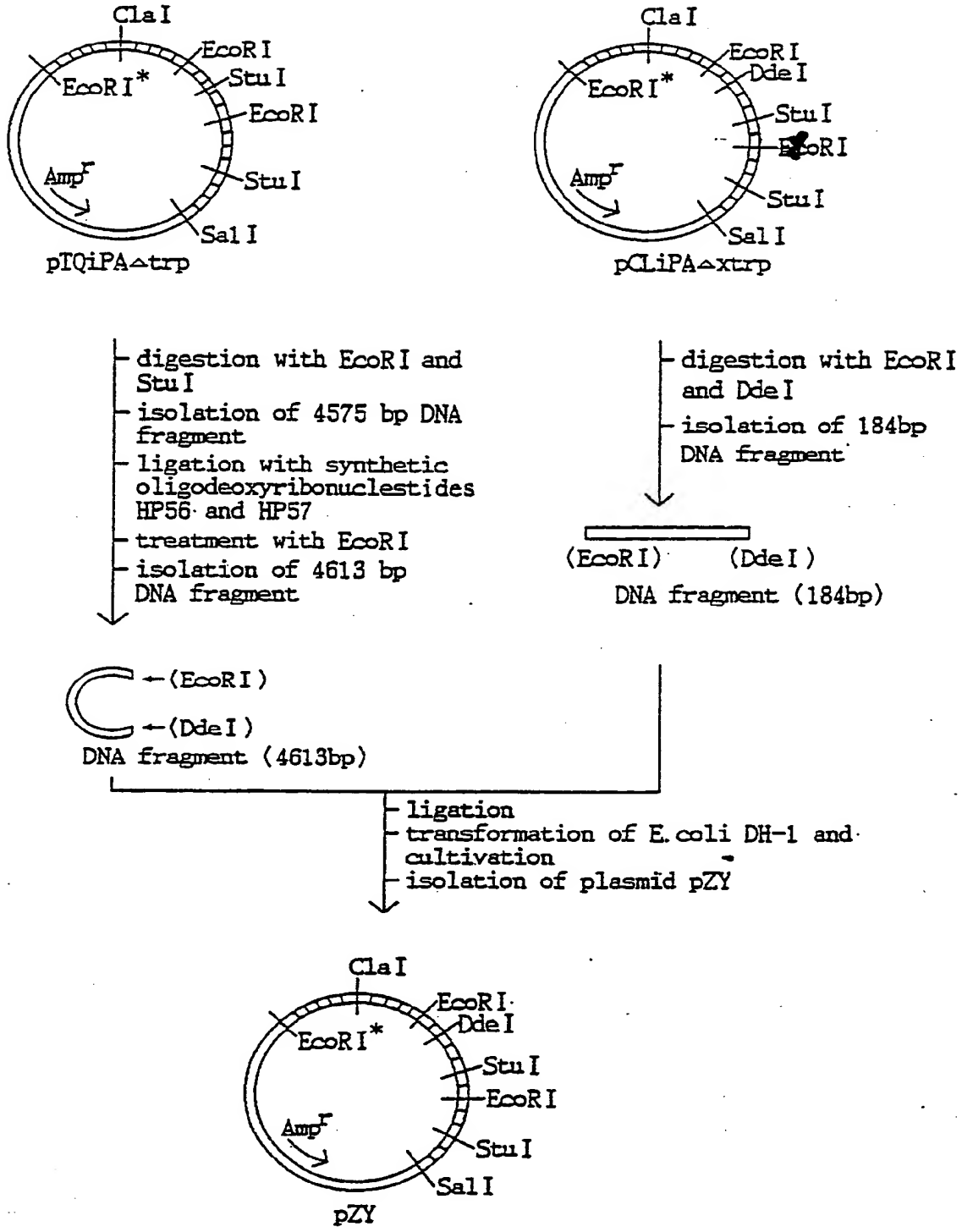
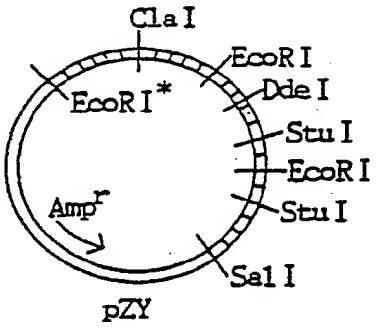
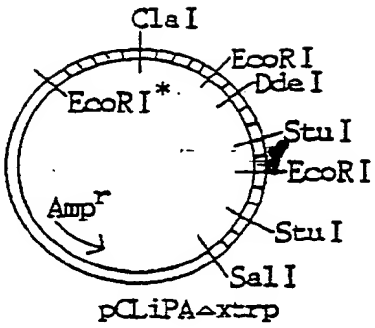
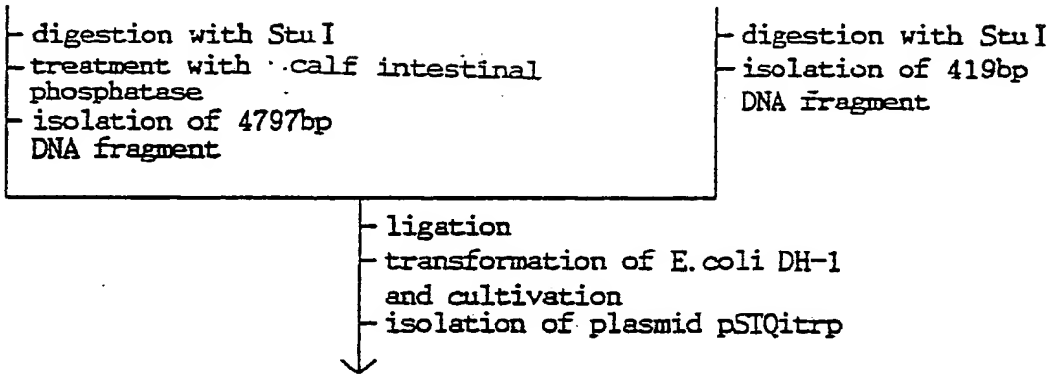


Fig. 14 Construction and cloning of plasmid pSTQitrp







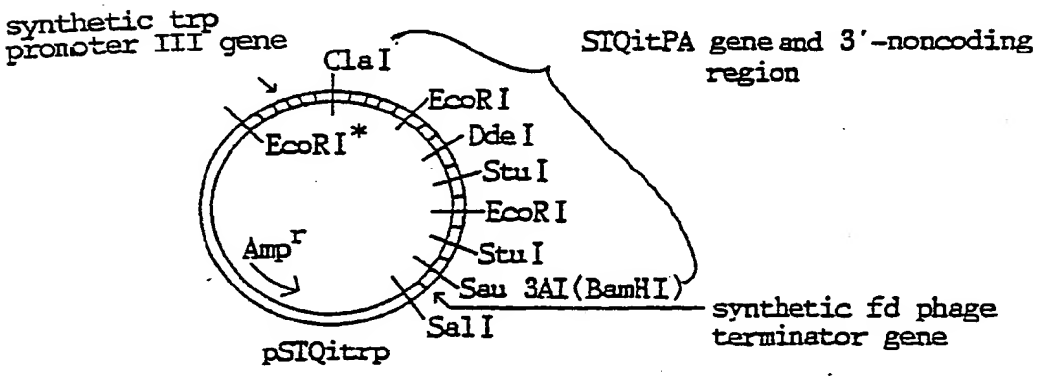


Fig. 15 Construction and cloning of plasmid pSTQktrp

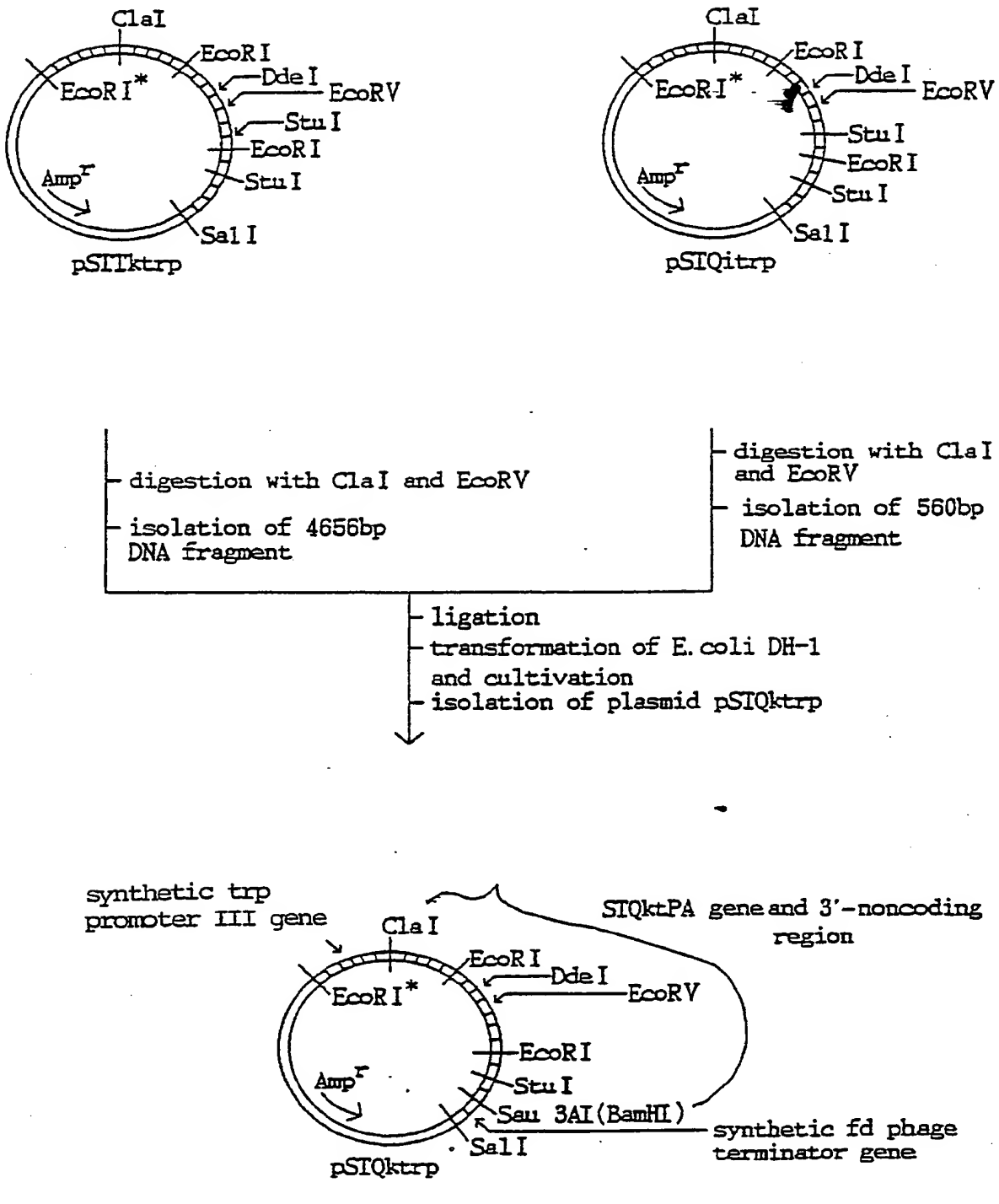


Fig. 16 Construction and cloning of plasmid pMH9006

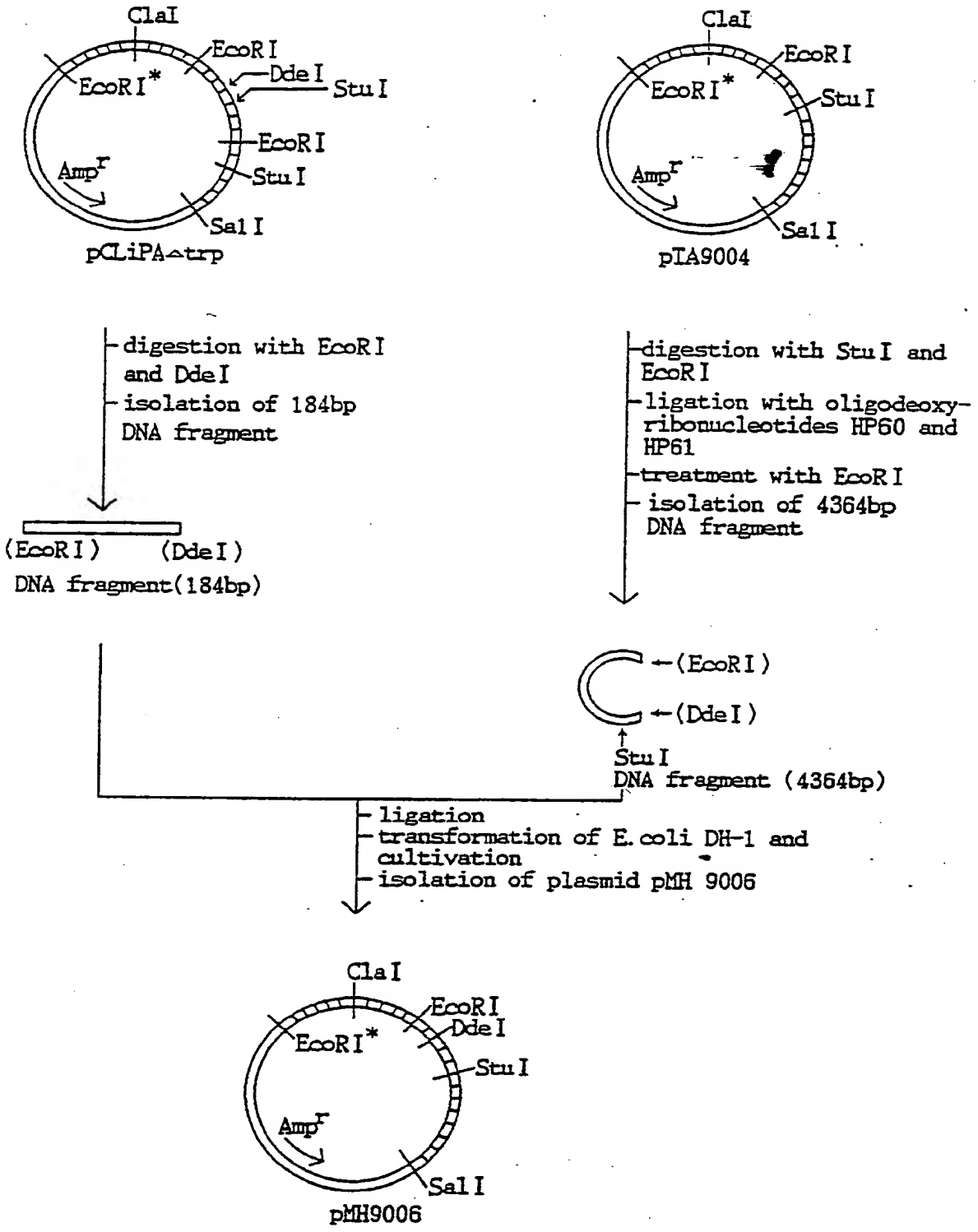


Fig. 17 Construction and cloning of plasmid pthITtrp

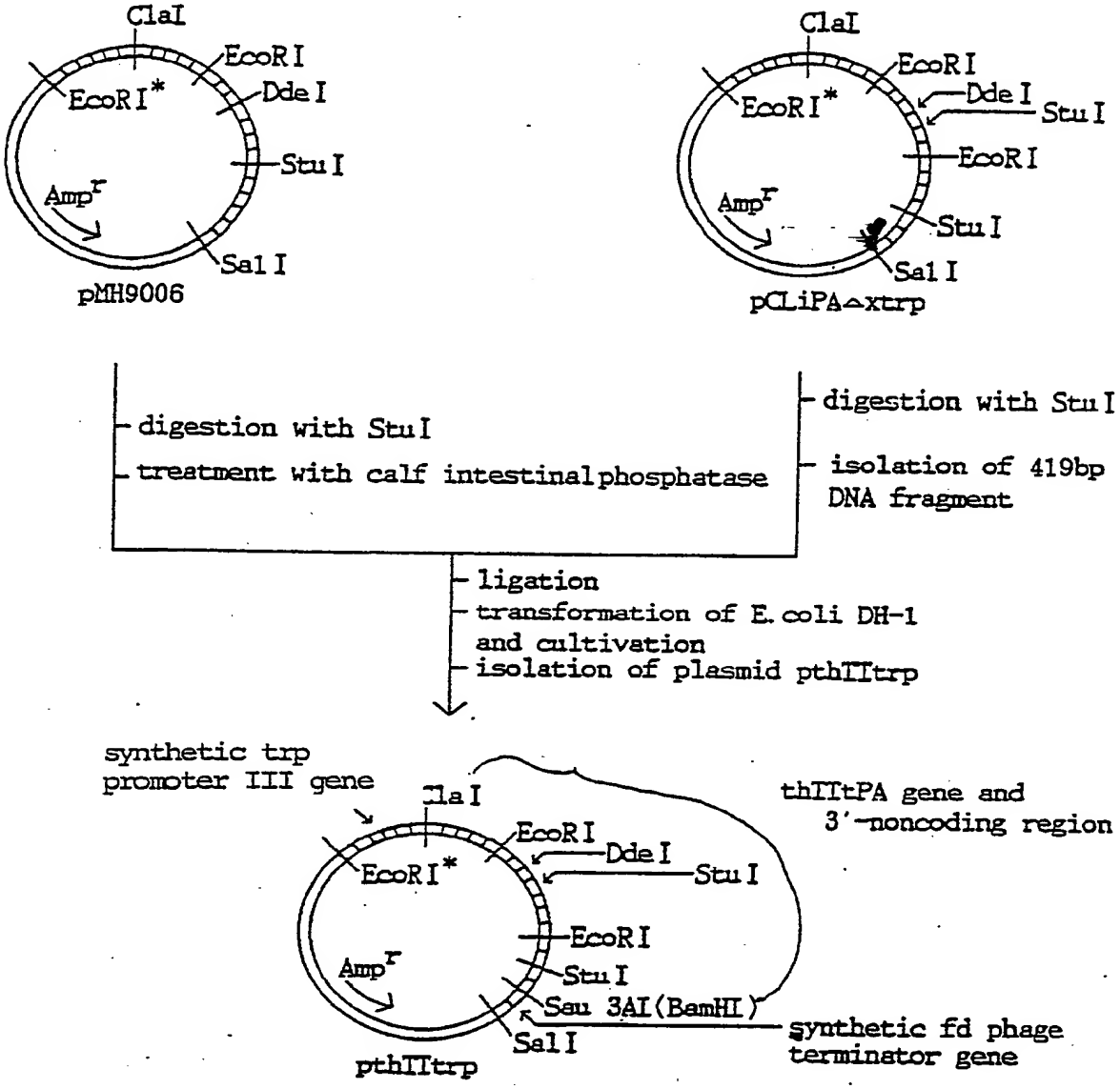


Fig. 18 Construction and cloning of plasmid pMH9007

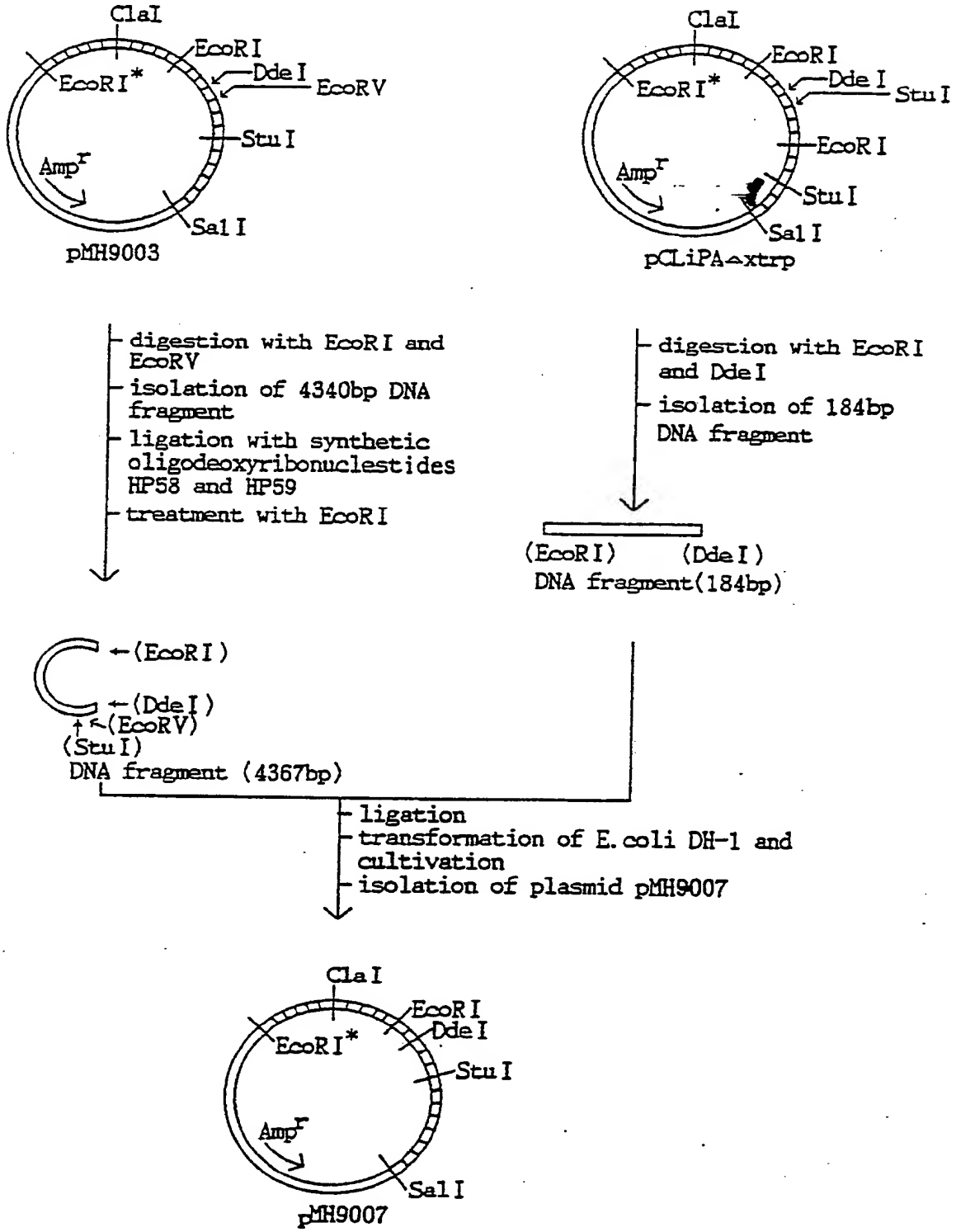


Fig. 19 Construction and cloning of plasmid puITtrp

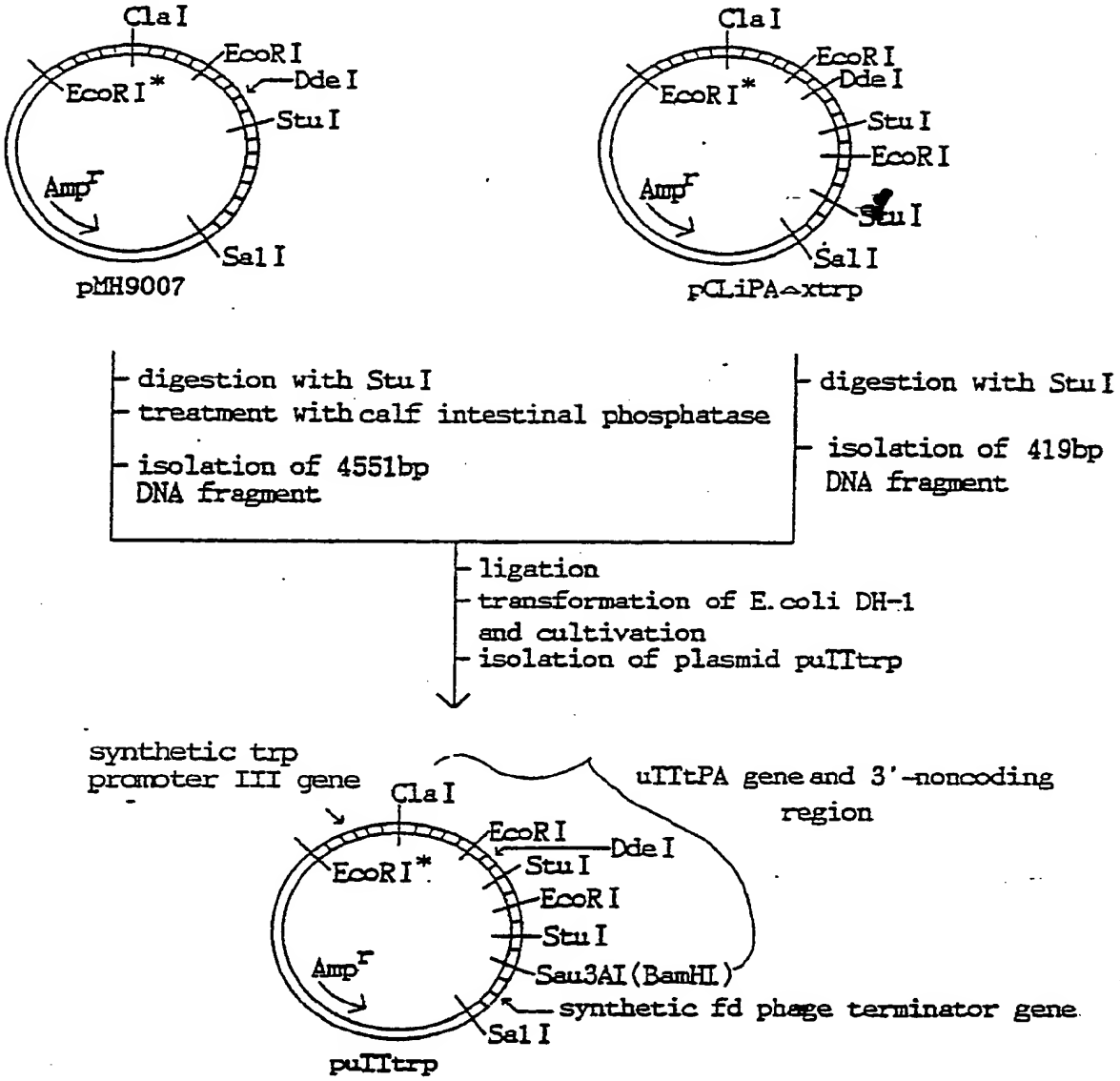


Fig. 20. Construction and cloning of plasmid pST118

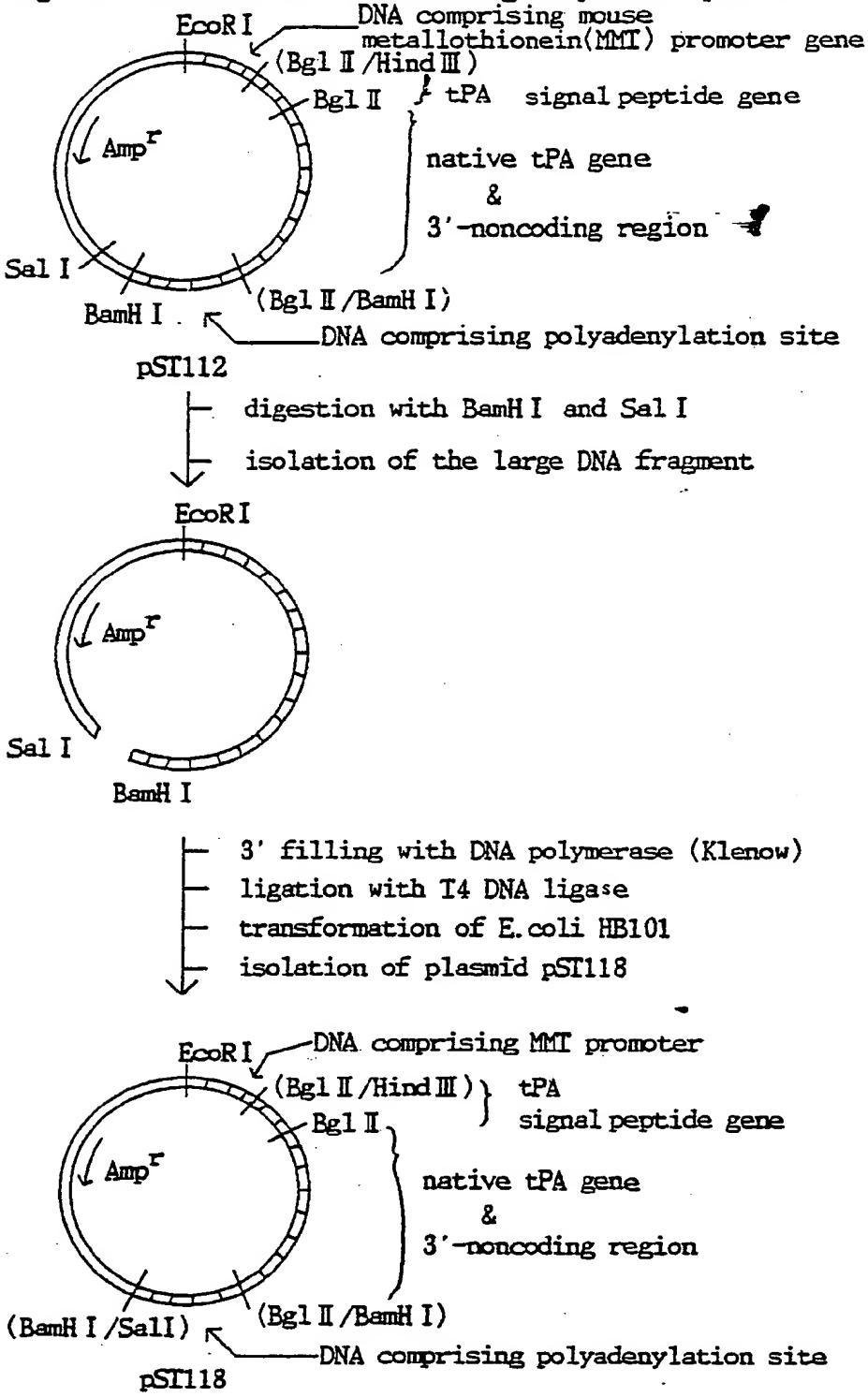


Fig. 21-(1). cDNA sequence of a native tPA in PST112
(Upper: Coding chain
Lower: Coded amino acid sequence)

```
                10          20          30          40          50          60
5'- GTTAAGGGACGCTGTGAAGCAATCATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTG
                                MetAspAlaMetLysArgGlyLeuCysCysValLeu

                70          80          90          100         110         120
CTGCTGTGTGGAGCAGTCTTCGTTTCGCCCAGCCAGGAAATCCATGCCCGATTCAGAAGA
LeuLeuCysGlyAlaValPheValSerProSerGlnGluIleHisAlaArgPheArgArg

               130         140         150         160         170         180
GGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAAACGCAGATGATATACCAGCAA
GlyAlaArgSerTyrGlnValIleCysArgAspGluLysThrGlnMetIleTyrGlnGln
          native tPA
       190         200         210         220         230         240
CATCAGTCATGGCTGCGCCCTGTGCTCAGAAGCAACCGGGTGGAATATTGCTGGTGCAAC
HisGlnSerTrpLeuArgProValLeuArgSerAsnArgValGluTyrCysTrpCysAsn

               250         260         270         280         290         300
AGTGGCAGGGCACAGTGCCACTCAGTGCCTGTCAAAAGTTGCAGCGAGCCAAGGTGTTTC
SerGlyArgAlaGlnCysHisSerValProValLysSerCysSerGluProArgCysPhe

               310         320         330         340         350         360
AACGGGGGCACCTGCCAGCAGGCCCTGTACTTCTCAGATTTCGTGTGCCAGTGCCCCGAA
AsnGlyGlyThrCysGlnGlnAlaLeuTyrPheSerAspPheValCysGlnCysProGlu

               370         380         390         400         410         420
GGATTTGCTGGGAAGTGCTGTGAAATAGATACCAGGGCCACGTGCTACGAGGACCAGGGC
GlyPheAlaGlyLysCysCysGluIleAspThrArgAlaThrCysTyrGluAspGlnGly

               430         440         450         460         470         480
ATCAGCTACAGGGGCACGTGGAGCACAGCGGAGAGTGGCGCCGAGTGCACCAACTGGAAC
IleSerTyrArgGlyThrTrpSerThrAlaGluSerGlyAlaGluCysThrAsnTrpAsn

               490         500         510         520         530         540
AGCAGCGCGTTGGCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGGGC
SerSerAlaLeuAlaGlnLysProTyrSerGlyArgArgProAspAlaIleArgLeuGly

               550         560         570         580         590         600
CTGGGGAACCACAACTACTGCAGAAACCCAGATCGAGACTCAAAGCCCTGGTGCTACGTC
LeuGlyAsnHisAsnTyrCysArgAsnProAspArgAspSerLysProTrpCysTyrVal

               610         620         630         640         650         660
TTTAAGGCGGGGAAGTACAGCTCAGAGTTCTGCAGCACCCCTGCCTGCTCTGAGGGAAAC
PheLysAlaGlyLysTyrSerSerGluPheCysSerThrProAlaCysSerGluGlyAsn

               670         680         690         700         710         720
AGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCG
SerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHisSerLeuThrGluSer

               730         740         750         760         770         780
GGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTTTACACAGCACAG
GlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLysValTyrThrAlaGln

               790         800         810         820         830         840
AACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGGAATCCTGATGGG
AsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArgAsnProAspGly

               850         860         870         880         890         900
GATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTACTGTGAT
AspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrpGluTyrCysAsp

               910         920         930         940         950         960
GTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAA
ValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnProGlnPheArgIleLys

               970         980         990        1000        1010        1020
GGAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCTTTGCCAAGCAC
GlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIlePheAlaLysHis

              1030        1040        1050        1060        1070        1080
AGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATCAGCTCCTGCTGGATT
ArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSerSerCysTrpIle
```

Fig. 21-(2).

```
      1090       1100       1110       1120       1130       1140
CTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTG
LeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeuThrValIleLeu

      1150       1160       1170       1180       1190       1200
GGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAATAC
GlyArgThrTyrArgValValProGlyGluGluGluGlnLysPheGluValGluLysTyr

      1210       1220       1230       1240       1250       1260
ATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCGCTGCTGCAGCTG
IleValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAlaLeuLeuGlnLeu

      1270       1280       1290       1300       1310       1320
AAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACTGTGTGCCTTCCC
LysSerAspSerSerArgCysAlaGlnGluSerSerValValArgThrValCysLeuPro

      1330       1340       1350       1360       1370       1380
CCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCAT
ProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGlyTyrGlyLysHis

      1390       1400       1410       1420       1430       1440
GAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCA
GluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisValArgLeuTyrPro

      1450       1460       1470       1480       1490       1500
TCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGT
SerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAspAsnMetLeuCys

      1510       1520       1530       1540       1550       1560
GCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTGCACGACGCCTGCCAGGGCGAT
AlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAlaCysGlnGlyAsp

      1570       1580       1590       1600       1610       1620
TCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGC
SerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuValGlyIleIleSer

      1630       1640       1650       1660       1670       1680
TGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAGGTTACCAACTAC
TrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLysValThrAsnTyr

      1690       1700       1710       1720       1730       1740
CTAGACTGGATTCGTGACAACATGCGACCGTGACCAGGAACACCCGACTCCTCAAAAGCA
LeuAspTrpIleArgAspAsnMetArgPro***

      1750       1760       1770       1780       1790       1800
AATGAGATCCCGCCTCTTCTTCTTCAGAAGACACTGCAAAGGCGCAGTGCTTCTCTACAG

      1810       1820       1830       1840       1850       1860
ACTTCTCCAGACCCACCACACCGCAGAAGCGGGACGAGACCCTACAGGAGAGGGAAGAGT

      1870       1880       1890       1900       1910       1920
GCATTTTCCCAGATACTTCCCATTTTGGAAGTTTTCAGGACTTGGTCTGATTTCAGGATA

      1930       1940       1950       1960       1970       1980
CTCTGTCAGATGGGAAGACATGAATGCACACTAGCCTCTCCAGGAATGCCTCCTCCCTGG

      1990       2000       2010       2020       2030       2040
GCAGAAGTGGCCATGCCACCCTGTTTTCGCTAAAGCCCAACCTCCTGACCTGTCACCGTG

      2050       2060       2070       2080       2090       2100
AGCAGCTTTGGAAACAGGACCACAAAAATGAAAGCATGTCTCAATAGTAAAAGAAACAAG

A -3'
```

Fig. 22. Construction and cloning of plasmid pmIQk118

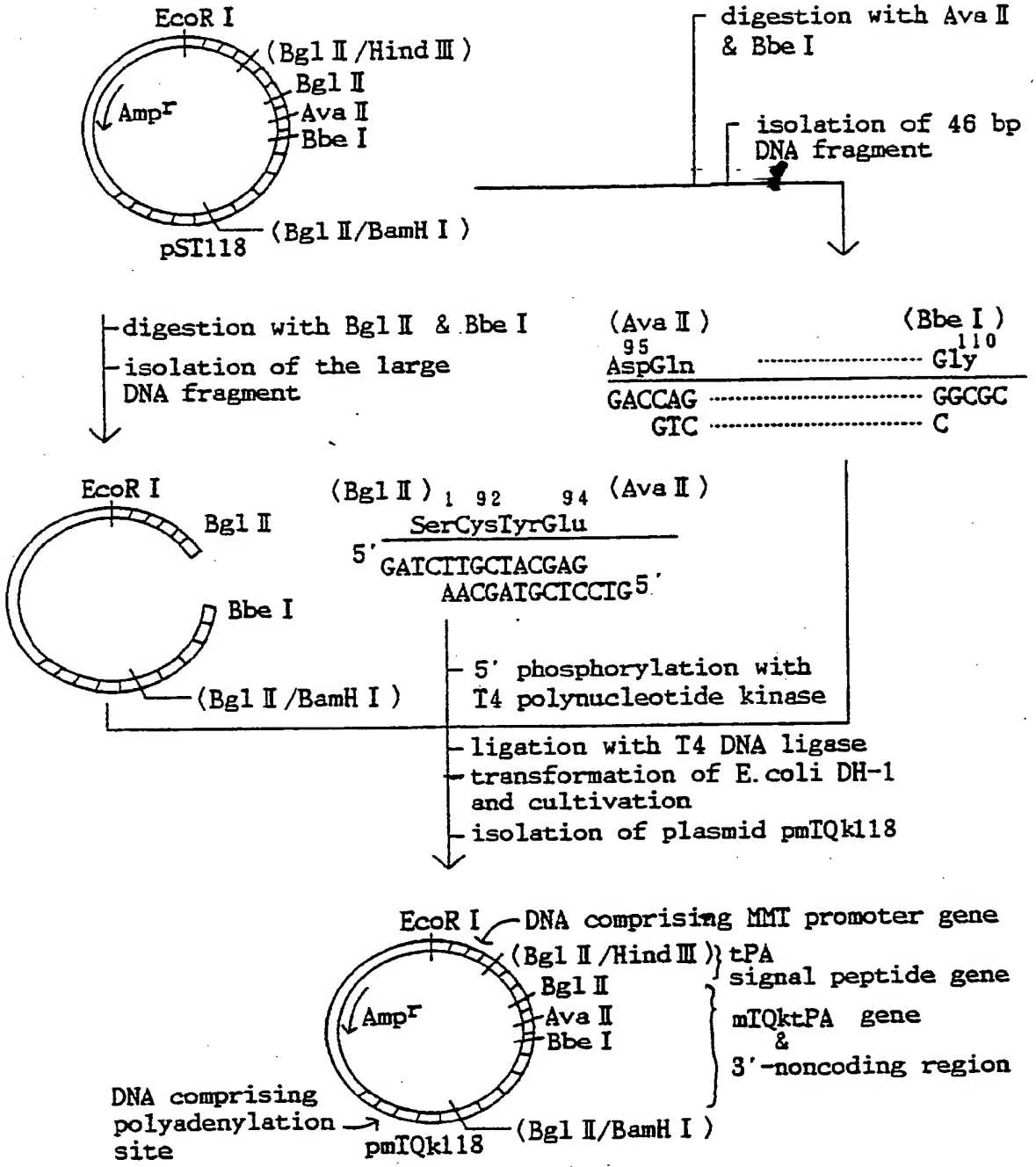


Fig. 23. Construction and cloning of plasmid pmTQk112

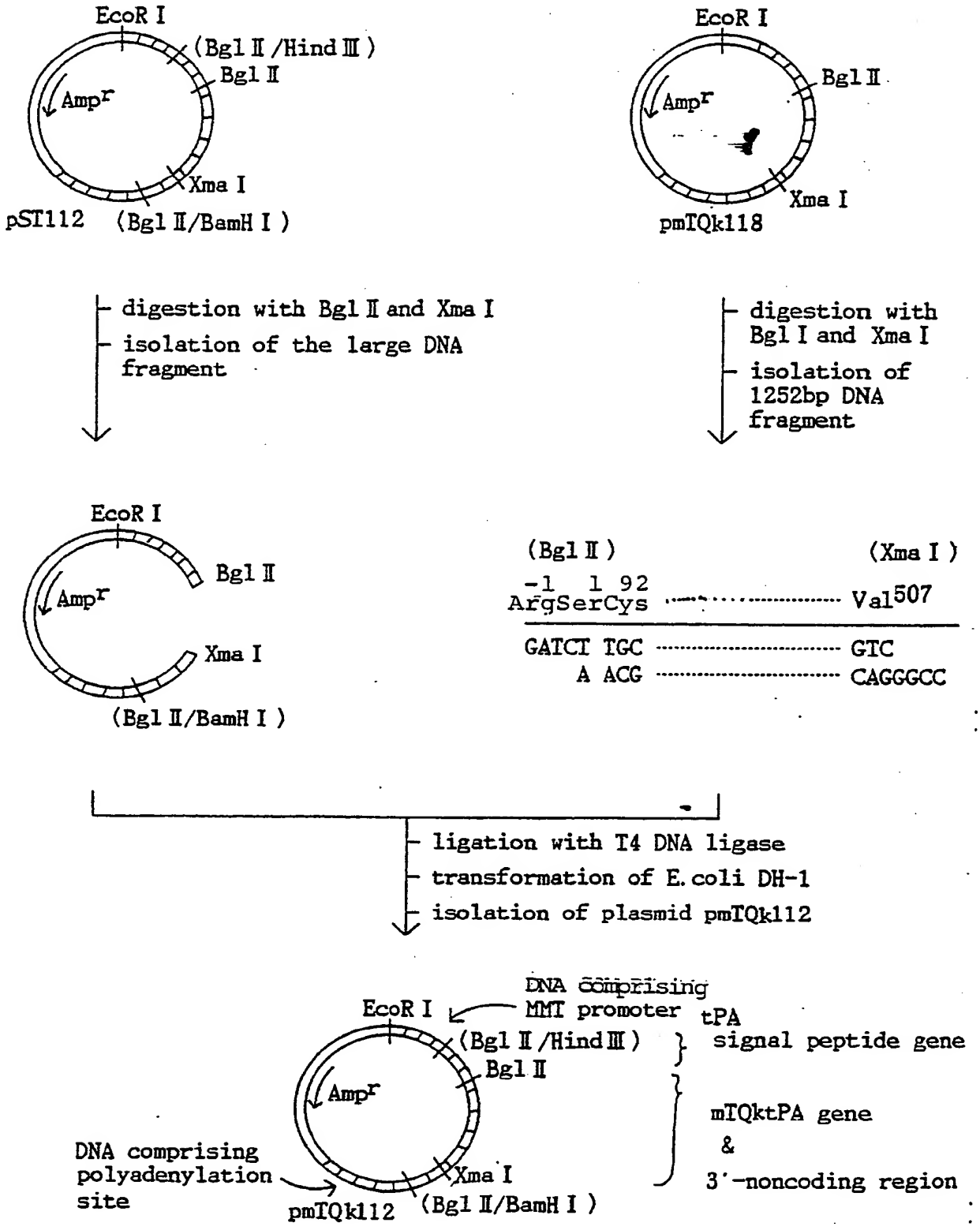


Fig. 24. Construction and cloning of plasmid pHS9006

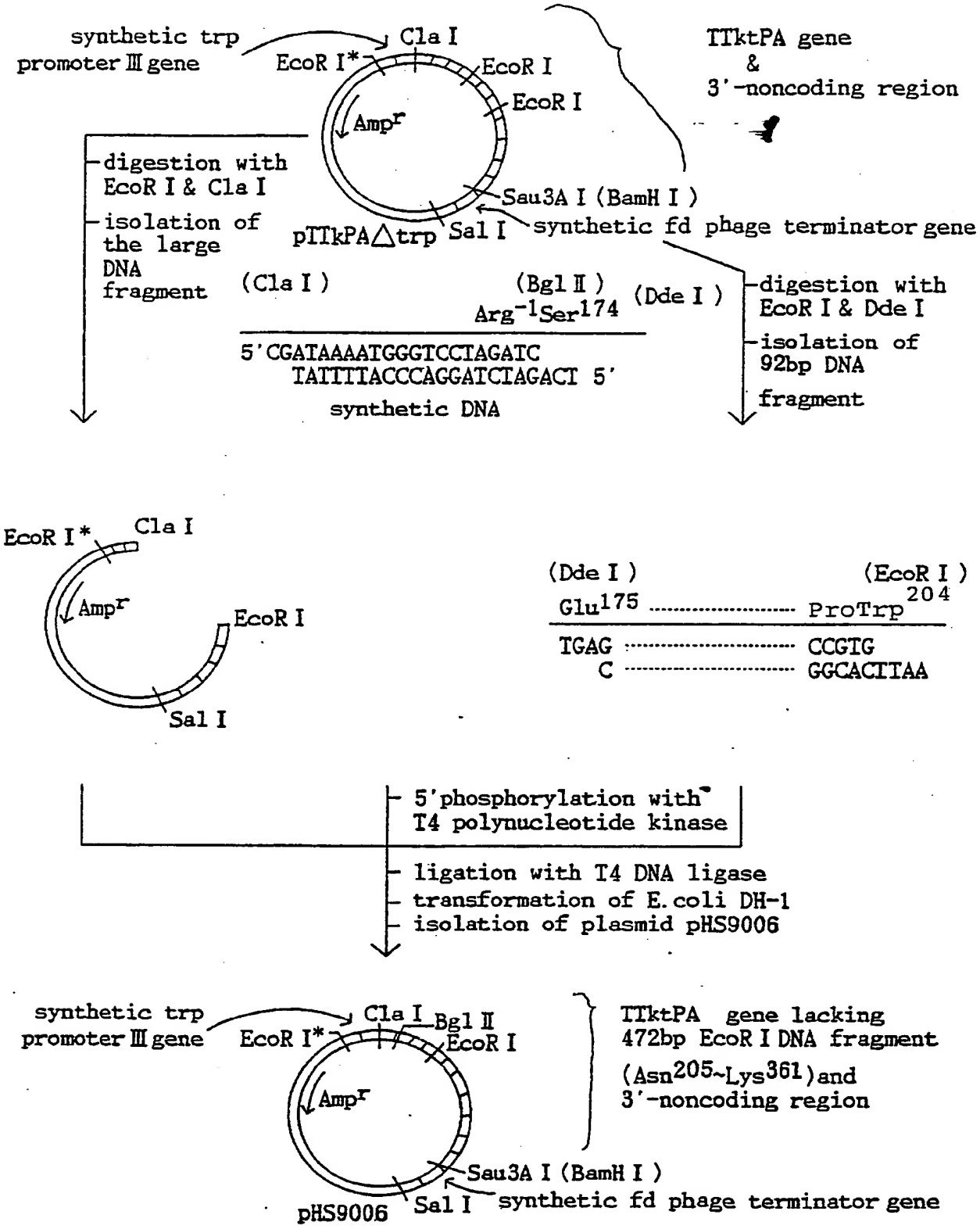


Fig. 25. Construction and cloning of plasmid pHS3020

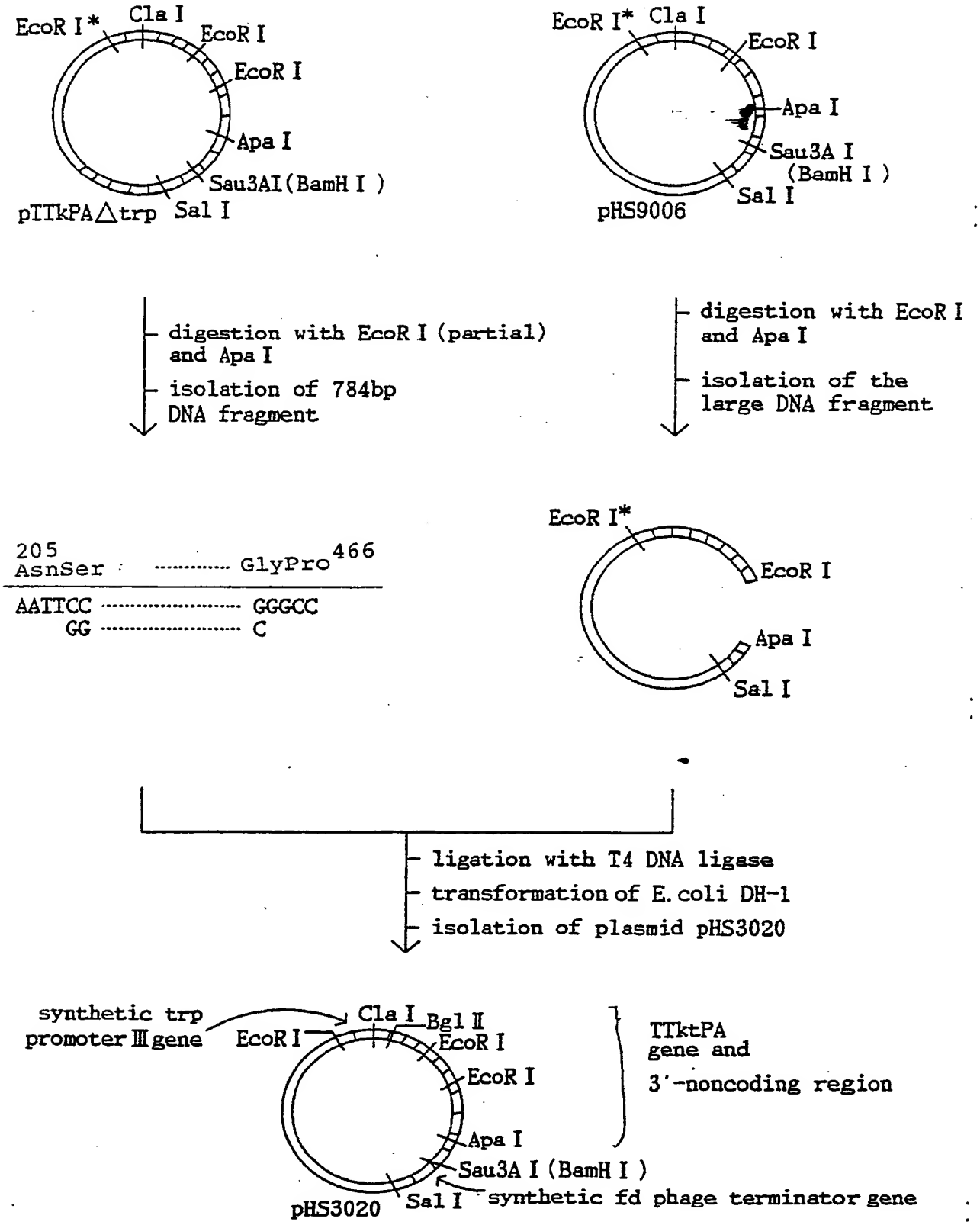


Fig. 26. Construction and cloning of plasmid pmTTk

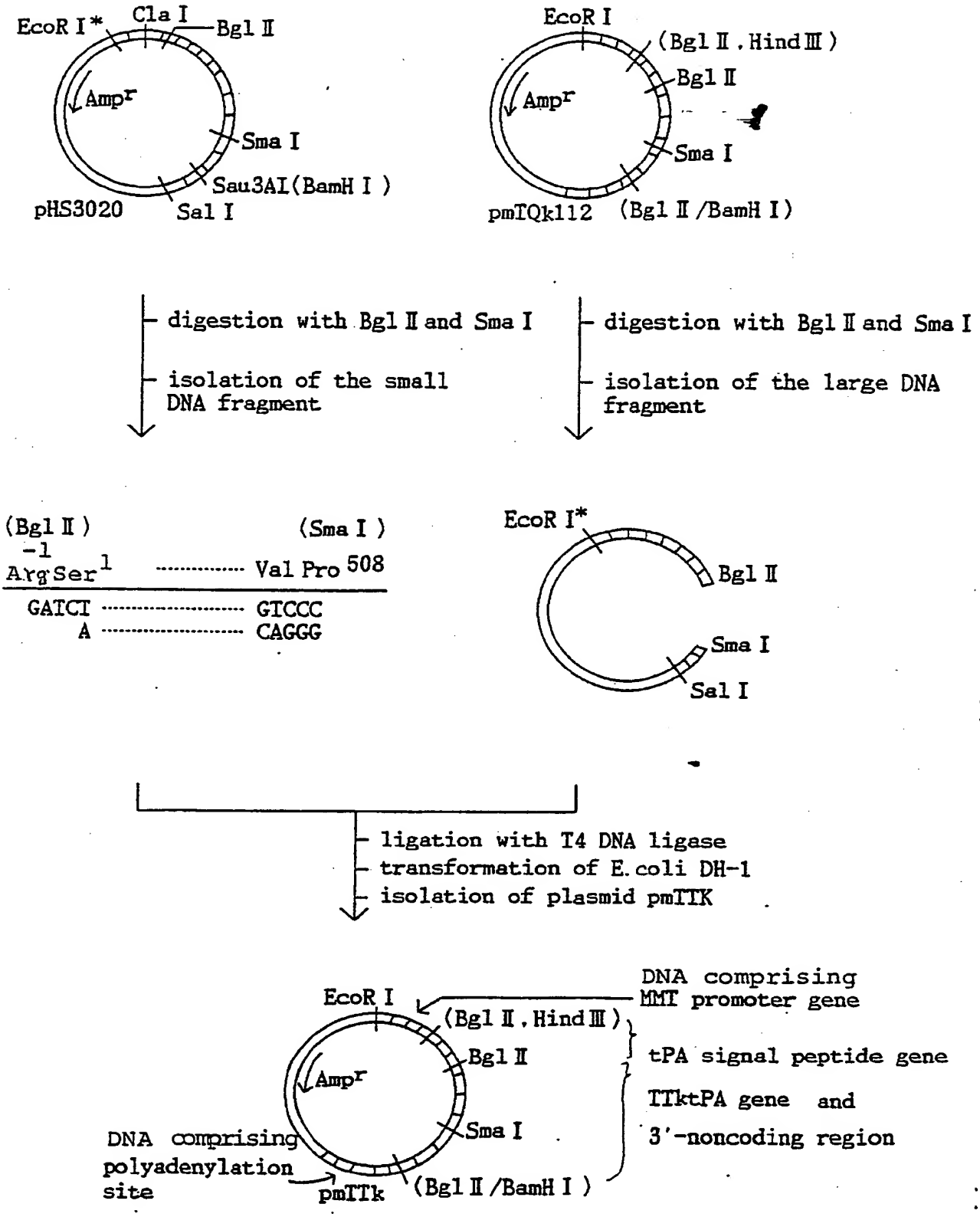


Fig. 27. Construction and cloning of plasmid pMH3025

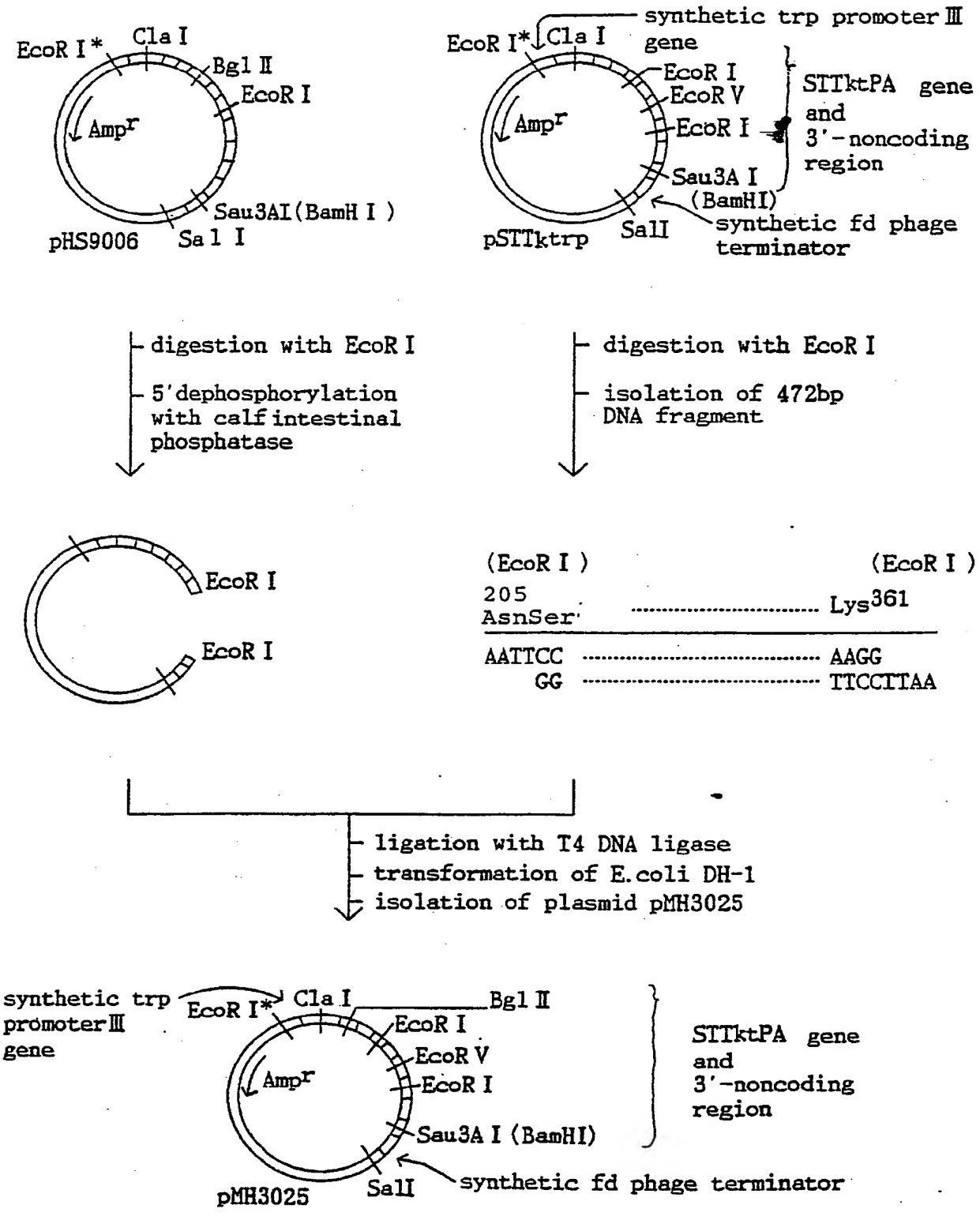


Fig. 28. Construction and cloning of plasmid pmSTIk

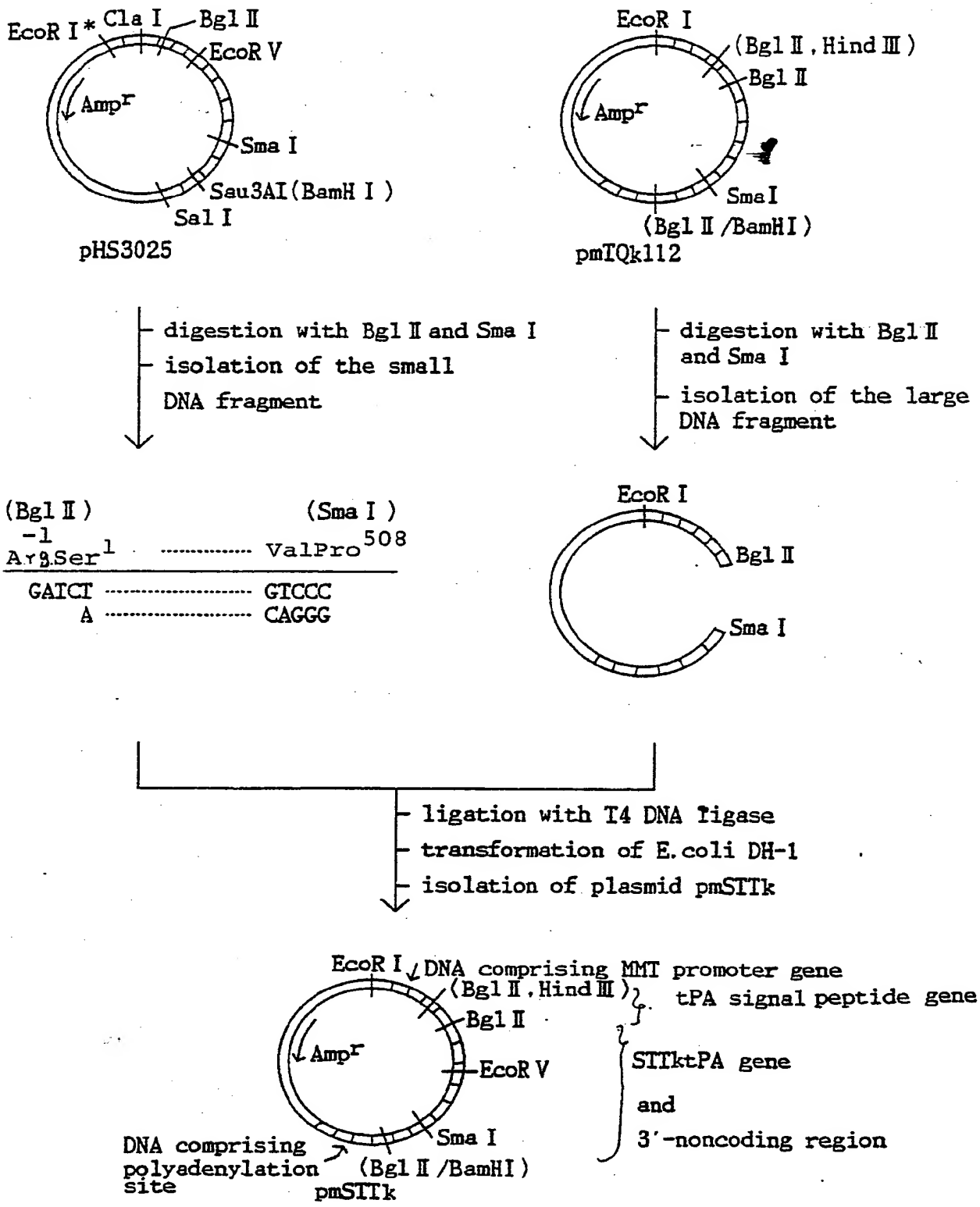


Fig. 29. DNA Sequence of coding region in pTTkPAΔtrp

(Upper: Coding chain
Lower: Coded amino acid sequence)

SEQ ID NO:1

5,840,533 US version of this document

```
                10        20        30        40        50        60
5'-ATGTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGCAC
  MetSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHis
  |→  TTk-tPA

                70        80        90       100       110       120
AGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAG
SerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLys

               130       140       150       160       170       180
GTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGC
ValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCys

               190       200       210       220       230       240
CGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACG
ArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThr

               250       260       270       280       290       300
TGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGCCT
TrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnPro

               310       320       330       340       350       360
CAGTTTCGCATCAAAGGAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCC
GlnPheArgIleLysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAla

               370       380       390       400       410       420
ATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATC
IlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIle

               430       440       450       460       470       480
AGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCAC
SerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHis

               490       500       510       520       530       540
CTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTT
LeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGlnLysPhe

               550       560       570       580       590       600
GAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATT
GluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIle

               610       620       630       640       650       660
GCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGC
AlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArg

               670       680       690       700       710       720
ACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCC
ThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSer

               730       740       750       760       770       780
GGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCAT
GlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHis

               790       800       810       820       830       840
GTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACC
ValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThr

               850       860       870       880       890       900
GACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGGCCCCAGGCAAACTTGCACGAC
AspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAsp

               910       920       930       940       950       960
GCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTG
AlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeu

              970       980       990      1000      1010      1020
GTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACA
ValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThr

             1030      1040      1050      1060      1070
AAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA -3'
LysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
                                                  ↤
```

Fig. 30. DNA sequence of coding region in pTTiPAΔtrp

(Upper: Coding chain
Lower: Coded amino acid sequence)

```
                10          20          30          40          50          60
5'-  ATGTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGCAC
     MetSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHis
        ↦TTitPA
                70          80          90          100         110         120
     AGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAG
     SerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLys

            130         140         150         160         170         180
     GTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGC
     ValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCys

            190         200         210         220         230         240
     CGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACG
     ArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThr

            250         260         270         280         290         300
     TGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGCCT
     TrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnPro

            310         320         330         340         350         360
     CAGTTTCGCATCATAGGAGGCCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCC
     GlnPheArgIleIleGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAla

            370         380         390         400         410         420
     ATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATC
     IlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIle

            430         440         450         460         470         480
     AGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCAC
     SerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHis

            490         500         510         520         530         540
     CTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTT
     LeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGlnLysPhe

            550         560         570         580         590         600
     GAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATT
     GluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIle

            610         620         630         640         650         660
     GCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGC
     AlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArg

            670         680         690         700         710         720
     ACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCC
     ThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSer

            730         740         750         760         770         780
     GGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCAT
     GlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHis

            790         800         810         820         830         840
     GTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACC
     ValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThr

            850         860         870         880         890         900
     GACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTGCACGAC
     AspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAsp

            910         920         930         940         950         960
     GCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTG
     AlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeu

            970         980         990         1000        1010        1020
     GTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACA
     ValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThr

           1030        1040        1050        1060        1070
     AAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA -3'
     LysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
                                                    ↤
```

Fig. 31. DNA sequence of coding region in pTQkPAΔtrp
(Upper: Coding chain, Lower: Coded amino acid sequence)

```
          10         20         30         40         50         60
5'- ATGTGTTATGAGGACCAGGGCATCAGCTACAGGGGCACGTGGAGCACAGCGGAGAGTGGC
    MetCysTyrGluAspGlnGlyIleSerTyrArgGlyThrTrpSerThrAlaGluSerGly
       ↦ TQKtPA
          70         80         90        100        110        120
    GCCGAGTGCACCAACTGGAACAGCAGCGCGTTGGCCCAGAAGCCCTACAGCGGGCGGAGG
    AlaGluCysThrAsnTrpAsnSerSerAlaLeuAlaGlnLysProTyrSerGlyArgArg

         130        140        150        160        170        180
    CCAGACGGCATCAGGCTGGGCCTGGGGAACCACAACTACTGCAGAAACCCAGATCGAGAC
    ProAspAlaIleArgLeuGlyLeuGlyAsnHisAsnTyrCysArgAsnProAspArgAsp

         190        200        210        220        230        240
    TCAAAGCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCTGCAGCACC
    SerLysProTrpCysTyrValPheLysAlaGlyLysTyrSerSerGluPheCysSerThr

         250        260        270        280        290        300
    CCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGC
    ProAlaCysSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGly

         310        320        330        340        350        360
    ACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATA
    ThrHisSerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIle

         370        380        390        400        410        420
    GGCAAGGTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAAT
    GlyLysValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsn

         430        440        450        460        470        480
    TACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGG
    TyrCysArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArg

         490        500        510        520        530        540
    CTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGC
    LeuThrTrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSer

         550        560        570        580        590        600
    CAGCCTCAGTTTCGCATCAAAGGAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAG
    GlnProGlnPheArgIleLysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGln

         610        620        630        640        650        660
    GCTGCCATCTTTGCCAAGCACAGGAGGTCGCCCCGGAGAGCGGTTCCTGTGCGGGGGCATA
    AlaAlaIlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIle

         670        680        690        700        710        720
    CTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCC
    LeuIleSerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProPro

         730        740        750        760        770        780
    CACCACCTGACGGTGATCTTGGGCAGAACATACCCGGTGGTCCCTGGCGAGGAGGAGCAG
    HisHisLeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGln

         790        800        810        820        830        840
    AAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAAT
    LysPheGluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsn

         850        860        870        880        890        900
    GACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTG
    AspIleAlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerVal

         910        920        930        940        950        960
    GTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAG
    ValArgThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGlu

         970        980        990       1000       1010       1020
    CTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAG
    LeuSerGlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGlu

        1030       1040       1050       1060       1070       1080
    GCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACA
    AlaHisValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThr

        1090       1100       1110       1120       1130       1140
    GTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTG
    ValThrAspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeu

        1150       1160       1170       1180       1190       1200
    CACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATG
    HisAspAlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMet

        1210       1220       1230       1240       1250       1260
    ACTTTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTG
    ThrLeuValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyVal

        1270       1280       1290       1300       1310
    TACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA-3'
    TyrThrLysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
                                                        ↤
```

Fig. 32. DNA sequence of coding region in pTQiPAΔtrp

(Upper: Coding chain, Lower: Coded amino acid sequence)

```
          10         20         30         40         50         60
5'-ATGTGTTATGAGGACCAGGGCATCAGCTACAGGGGCACGTGGAGCACAGCGGAGAGTGGC
  MetCysTyrGluAspGlnGlyIleSerTyrArgGlyThrTrpSerThrAlaGluSerGly
     ↦ TQitPA
          70         80         90        100        110        120
GCCGAGTGCACCAACTGGAACAGCAGCGCGTTGGCCCAGAAGCCCTACAGCGGGCGGAGG
AlaGluCysThrAsnTrpAsnSerSerAlaLeuAlaGlnLysProTyrSerGlyArgArg

         130        140        150        160        170        180
CCAGACGCCATCAGGCTGGGCCTGGGGAACCACAACTACTGCAGAAACCCAGATCGAGAC
ProAspAlaIleArgLeuGlyLeuGlyAsnHisAsnTyrCysArgAsnProAspArgAsp

         190        200        210        220        230        240
TCAAAGCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCTGCAGCACC
SerLysProTrpCysTyrValPheLysAlaGlyLysTyrSerSerGluPheCysSerThr

         250        260        270        280        290        300
CCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGC
ProAlaCysSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGly

         310        320        330        340        350        360
ACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATA
ThrHisSerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIle

         370        380        390        400        410        420
GGCAAGGTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAAT
GlyLysValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsn

         430        440        450        460        470        480
TACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGG
TyrCysArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArg

         490        500        510        520        530        540
CTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGC
LeuThrTrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSer

         550        560        570        580        590        600
CAGCCTCAGTTTCGCATCATAGGAGGCCTCTTCGCCGACATCGCCTCCCACCCCTGGCAG
GlnProGlnPheArgIleIleGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGln

         610        620        630        640        650        660
GCTGCCATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATA
AlaAlaIlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIle

         670        680        690        700        710        720
CTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCC
LeuIleSerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProPro

         730        740        750        760        770        780
CACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAG
HisHisLeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGlnGln

         790        800        810        820        830        840
AAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAAT
LysPheGluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsn

         850        860        870        880        890        900
GACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTG
AspIleAlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerVal

         910        920        930        940        950        960
GTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAG
ValArgThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGlu

         970        980        990       1000       1010       1020
CTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAG
LeuSerGlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGlu

        1030       1040       1050       1060       1070       1080
GCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACA
AlaHisValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThr

        1090       1100       1110       1120       1130       1140
GTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTG
ValThrAspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeu

        1150       1160       1170       1180       1190       1200
CACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATG
HisAspAlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMet

        1210       1220       1230       1240       1250       1260
ACTTTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTG
ThrLeuValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyVal

        1270       1280       1290       1300       1310
TACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA-3'
TyrThrLysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
                                                    ↤
```

Fig. 33. DNA sequence of coding region in pSTTktrp
(Upper: Coding chain
Lower: Coded amino acid sequence)

```
          10         20         30         40         50         60
5'-ATGTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGGCTACCGTGGCACGCAC
  MetSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHis
     → STTktPA
          70         80         90        100        110        120
AGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAG
SerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLys

         130        140        150        160        170        180
GTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGC
ValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCys

         190        200        210        220        230        240
CGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACG
ArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThr

         250        260        270        280        290        300
TGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGCCA
TrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnPro

         310        320        330        340        350        360
CAGTTTGATATCAAAGGAGGCCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCC
GlnPheAspIleLysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAla

         370        380        390        400        410        420
ATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCGTGTGCGGGGGCATACTCATC
IlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIle

         430        440        450        460        470        480
AGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCAC
SerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHis

         490        500        510        520        530        540
CTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTT
LeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGlnLysPhe

         550        560        570        580        590        600
GAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATT
GluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIle

         610        620        630        640        650        660
GCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGC
AlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArg

         670        680        690        700        710        720
ACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCC
ThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSer

         730        740        750        760        770        780
GGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCAT
GlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHis

         790        800        810        820        830        840
GTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACC
ValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThr

         850        860        870        880        890        900
GACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTGCACGAC
AspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAsp

         910        920        930        940        950        960
GCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTG
AlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeu

         970        980        990       1000       1010       1020
GTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACA
ValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThr

        1030       1040       1050       1060       1070
AAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA -3'
LysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
                                                  ←
```

Fig. 34. DNA sequence of coding region in pSTQktrp
(Upper: Coding chain
Lower: Coded amino acid sequence)

```
                10        20        30        40        50        60
5'-ATGTGTTATGAGGACCAGGGCATCAGCTACAGGGGCACGTGGAGCACAGCGGAGAGTGGC
   MetCysTyrGluAspGlnGlyIleSerTyrArgGlyThrTrpSerThrAlaGluSerGly
     ↦ STQKtpA
               70        80        90       100       110       120
   GCCGAGTGCACCAACTGGAACAGCAGCGCGTTGGCCCAGAAGCCCTACAGCGGGCGGAGG
   AlaGluCysThrAsnTrpAsnSerSerAlaLeuAlaGlnLysProTyrSerGlyArgArg

       130       140       150       160       170       180
   CCAGACGCCATCAGGCTGGGCCTGGGGAACCACAACTACTGCAGAAACCCAGATCGGGAC
   ProAspAlaIleArgLeuGlyLeuGlyAsnHisAsnTyrCysArgAsnProAspArgAsp

       190       200       210       220       230       240
   TCAAAGCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCTGCAGCACC
   SerLysProTrpCysTyrValPheLysAlaGlyLysTyrSerSerGluPheCysSerThr

       250       260       270       280       290       300
   CCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGC
   ProAlaCysSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGly

       310       320       330       340       350       360
   ACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATA
   ThrHisSerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIle

       370       380       390       400       410       420
   GGCAAGGTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAAT
   GlyLysValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsn

       430       440       450       460       470       480
   TACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGG
   TyrCysArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArg

       490       500       510       520       530       540
   CTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGC
   LeuThrTrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSer

       550       560       570       580       590       600
   CAGCCACAGTTTGATATCAAAGGAGGCCTGTTCGCCGACATCGCCTCCCACCCCTGGCAG
   GlnProGlnPheAspIleLysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGln

       610       620       630       640       650       660
   GCTGCCATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATA
   AlaAlaIlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIle

       670       680       690       700       710       720
   CTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCC
   LeuIleSerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProPro

       730       740       750       760       770       780
   CACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAG
   HisHisLeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGln

       790       800       810       820       830       840
   AAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAAT
   LysPheGluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsn

       850       860       870       880       890       900
   GACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTG
   AspIleAlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerVal

       910       920       930       940       950       960
   GTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAG
   ValArgThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGlu

       970       980       990      1000      1010      1020
   CTCTCCGGCTACGGCAAGCATGAGGCGTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAG
   LeuSerGlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGlu

      1030      1040      1050      1060      1070      1080
   GCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACA
   AlaHisValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThr

      1090      1100      1110      1120      1130      1140
   GTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTG
   ValThrAspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeu

      1150      1160      1170      1180      1190      1200
   CACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATG
   HisAspAlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMet

      1210      1220      1230      1240      1250      1260
   ACTTTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTG
   ThrLeuValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyVal

      1270      1280      1290      1300      1310
   TACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA-3'.
   TyrThrLysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
                                                    ↩
```

Fig. 35. DNA sequence of coding region in pSTQitrp
(Upper: Coding chain
Lower: Coded amino acid sequence)

```
                10         20         30         40         50         60
5'- ATGTGTTATGAGGACCAGGGCATCAGCTACAGGGGCACGTGGAGCACAGCGGAGAGTGGC
    MetCysTyrGluAspGlnGlyIleSerTyrArgGlyThrTrpSerThrAlaGluSerGly
      ↦ STQitPA
               70         80         90        100        110        120
    GCCGAGTGCACCAACTGGAACAGCAGCGGCGTTGGCCCAGAAGCCCTACAGCGGGCGGAGG
    AlaGluCysThrAsnTrpAsnSerSerAlaLeuAlaGlnLysProTyrSerGlyArgArg

              130        140        150        160        170        180
    CCAGACGCCATCAGGCTGGGCCTGGGGAACCACAACTACTGCAGAAACCCAGATCGAGAC
    ProAspAlaIleArgLeuGlyLeuGlyAsnHisAsnTyrCysArgAsnProAspArgAsp

              190        200        210        220        230        240
    TCAAAGCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCTGCAGCACC
    SerLysProTrpCysTyrValPheLysAlaGlyLysTyrSerSerGluPheCysSerThr

              250        260        270        280        290        300
    CCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGC
    ProAlaCysSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGly

              310        320        330        340        350        360
    ACGCACAGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATA
    ThrHisSerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIle

              370        380        390        400        410        420
    GGCAAGGTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAAT
    GlyLysValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsn

              430        440        450        460        470        480
    TACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGG
    TyrCysArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArg

              490        500        510        520        530        540
    CTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGC
    LeuThrTrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSer

              550        560        570        580        590        600
    CAGCCACAGTTTGATATCATAGGAGGCCTCTTCGCCGACATCGCCTCCCACCCCTGGCAG
    GlnProGlnPheAspIleIleGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGln

              610        620        630        640        650        660
    GCTGCCATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATA
    AlaAlaIlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIle

              670        680        690        700        710        720
    CTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCC
    LeuIleSerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProPro

              730        740        750        760        770        780
    CACCACCTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAG
    HisHisLeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGln

              790        800        810        820        830        840
    AAATTTGAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAAT
    LysPheGluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsn

              850        860        870        880        890        900
    GACATTGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTG
    AspIleAlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerVal

              910        920        930        940        950        960
    GTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAG
    ValArgThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGlu

              970        980        990       1000       1010       1020
    CTCTCCGGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAG
    LeuSerGlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGlu

             1030       1040       1050       1060       1070       1080
    GCTCATGTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACA
    AlaHisValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThr

             1090       1100       1110       1120       1130       1140
    GTCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTG
    ValThrAspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeu

             1150       1160       1170       1180       1190       1200
    CACGACGCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATG
    HisAspAlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMet

             1210       1220       1230       1240       1250       1260
    ACTTTGGTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTG
    ThrLeuValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyVal

             1270       1280       1290       1300       1310
    TACACAAAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA -3'
    TyrThrLysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
                                                          ↤
```

Fig. 36. DNA sequence of coding region in puTTtrp
(Upper: Coding chain
Lower: Coded amino acid sequence)

```
                10          20          30          40          50          60
5'-ATGTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGCAC
   MetSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHis
    ↳ uTT+PA

                70          80          90          100         110         120
AGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAG
SerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLys

        130         140         150         160         170         180
GTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGC
ValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCys

        190         200         210         220         230         240
CGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACG
ArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThr

        250         260         270         280         290         300
TGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGACTCTGCGTCCG
TrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnThrLeuArgPro

        310         320         330         340         350         360
CGGTTCAAAATCAAAGGAGGCCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCC
ArgPheLysIleLysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAla

        370         380         390         400         410         420
ATCTTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATC
IlePheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIle

        430         440         450         460         470         480
AGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCAC
SerSerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHis

        490         500         510         520         530         540
CTGACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTT
LeuThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGlnLysPhe

        550         560         570         580         590         600
GAAGTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATT
GluValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIle

        610         620         630         640         650         660
GCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGC
AlaLeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArg

        670         680         690         700         710         720
ACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCC
ThrValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSer

        730         740         750         760         770         780
GGCTACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCAT
GlyTyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHis

        790         800         810         820         830         840
GTCAGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACC
ValArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThr

        850         860         870         880         890         900
GACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGGCCCCAGGCAAACTTGCACGAC
AspAsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAsp

        910         920         930         940         950         960
GCCTGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTG
AlaCysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeu

        970         980         990         1000        1010        1020
GTGGGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACA
ValGlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThr

      1030        1040        1050        1060        1070
AAGGTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA -3'
LysValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
                                                  ↳
```

Fig. 37. DNA sequence of coding region in pthTTtrp

(Upper: Coding chain, Lower: Coded amino acid sequence)

```
          10         20         30         40         50         60
5'-ATGTCTGAGGGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGCAC
   MetSerGluGlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHis
     ↦ thTTtPA
         70         80         90        100        110        120
   AGCCTCACCGAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAG
   SerLeuThrGluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLys

        130        140        150        160        170        180
   GTTTACACAGCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGC
   ValTyrThrAlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCys

        190        200        210        220        230        240
   CGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACG
   ArgAsnProAspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThr

        250        260        270        280        290        300
   TGGGAGTACTGTGATGTGCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGCCA
   TrpGluTyrCysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnPro

        310        320        330        340        350        360
   ATTCCTAGATCTGGAGGCCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATC
   IleProArgSerGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIle

        370        380        390        400        410        420
   TTTGCCAAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATCAGC
   PheAlaLysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSer

        430        440        450        460        470        480
   TCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCACCTG
   SerCysTrpIleLeuSerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeu

        490        500        510        520        530        540
   ACGGTGATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAA
   ThrValIleLeuGlyArgThrTyrArgValValProGlyGluGluGluGlnLysPheGlu

        550        560        570        580        590        600
   GTCGAAAAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCG
   ValGluLysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAla

        610        620        630        640        650        660
   CTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACT
   LeuLeuGlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArgThr

        670        680        690        700        710        720
   GTGTGCCTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGC
   ValCysLeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGly

        730        740        750        760        770        780
   TACGGCAAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTC
   TyrGlyLysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisVal

        790        800        810        820        830        840
   AGACTGTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGAC
   ArgLeuTyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAsp

        850        860        870        880        890        900
   AACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTGCACGACGCC
   AsnMetLeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAla

        910        920        930        940        950        960
   TGCCAGGGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTG
   CysGlnGlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuVal

        970        980        990       1000       1010       1020
   GGCATCATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAG
   GlyIleIleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLys

       1030       1040       1050       1060
   GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA-3'
   ValThrAsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
                                                ↤
```

Fig. 38. DNA sequence of coding region in pmTQk112

(Upper: Coding chain
Lower: Coded amino acid sequence)

```
                10        20        30        40        50        60
5'- ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTT
    MetAspAlaMetLysArgGlyLeuCysCysValLeuLeuLeuCysGlyAlaValPheVal

                70        80        90        100       110       120
    TCGCCCAGCCAGGAAATCCATGCCCGATTCAGAAGAGGAGCCAGATCTTGCTACGAGGAC
    SerProSerGlnGluIleHisAlaArgPheArgArgGlyAlaArgSerCysTyrGluAsp
                                                  ⟶ mTQktPA
                130       140       150       160       170       180
    CAGGGCATCAGCTACAGGGGCACGTGGAGCACAGCGGAGAGTGGCGCCGAGTGCACAAAC
    GlnGlyIleSerTyrArgGlyThrTrpSerThrAlaGluSerGlyAlaGluCysThrAsn

                190       200       210       220       230       240
    TGGAACAGCAGCGCGTTGGCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGG
    TrpAsnSerSerAlaLeuAlaGlnLysProTyrSerGlyArgArgProAspAlaIleArg

                250       260       270       280       290       300
    CTGGGCCTGGGGAACCACAACTACTGCAGAAACCCAGATCGAGACTCAAAGCCCTGGTGC
    LeuGlyLeuGlyAsnHisAsnTyrCysArgAsnProAspArgAspSerLysProTrpCys

                310       320       330       340       350       360
    TACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCTGCAGCACCCCTGCCTGCTCTGAG
    TyrValPheLysAlaGlyLysTyrSerSerGluPheCysSerThrProAlaCysSerGlu

                370       380       390       400       410       420
    GGAAACAGTGACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGCACAGCCTCACC
    GlyAsnSerAspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHisSerLeuThr

                430       440       450       460       470       480
    GAGTCGGGTGCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTTTACACA
    GluSerGlyAlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLysValTyrThr

                490       500       510       520       530       540
    GCACAGAACCCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGGAATCCT
    AlaGlnAsnProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArgAsnPro.

                550       560       570       580       590       600
    GATGGGGATGCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTAC
    AspGlyAspAlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrpGluTyr

                610       620       630       640       650       660
    TGTGATGTGCCCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGC
    CysAspValProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnProGlnPheArg

                670       680       690       700       710       720
    ATCAAAGGAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCTTTGCC
    IleLysGlyGlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIlePheAla

                730       740       750       760       770       780
    AAGCACAGGAGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATCAGCTCCTGC
    LysHisArgArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSerSerCys

                790       800       810       820       830       840
    TGGATTCTCTCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCACCTGACGGTG
    TrpIleLeuSerAlaAlaHisCysPheGlnArgPheProProHisHisLeuThrVal

                850       860       870       880       890       900
    ATCTTGGGCAGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAA
    IleLeuGlyArgThrTyrArgValValProGlyGluGluGlnLysPheGluValGlu

                910       920       930       940       950       960
    AAATACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCGCTGCTG
    LysTyrIleValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAlaLeuLeu

                970       980       990       1000      1010      1020
    CAGCTGAAATCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACTGTGTGC
    GlnLeuLysSerAspSerSerArgCysAlaGlnGluSerSerValValArgThrValCys

                1030      1040      1050      1060      1070      1080
    CTTCCCCCGGCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGC
    LeuProProAlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGlyTyrGly

                1090      1100      1110      1120      1130      1140
    AAGCATGAGGCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTG
    LysHisGluAlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisValArgLeu

                1150      1160      1170      1180      1190      1200
    TACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATG
    TyrProSerSerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAspAsnMet

                1210      1220      1230      1240      1250      1260
    CTGTGTGCTGGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTGCACGACGCCTGCCAG
    LeuCysAlaGlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAlaCysGln

                1270      1280      1290      1300      1310      1320
    GGCGATTCGGGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATC
    GlyAspSerGlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuValGlyIle

                1330      1340      1350      1360      1370      1380
    ATCAGCTGGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAGGTTACC
    IleSerTrpGlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLysValThr

                1390      1400      1410      1420
    AACTACCTAGACTGGATTCGTGACAACATGCGACCGTGA -3'
    AsnTyrLeuAspTrpIleArgAspAsnMetArgPro***
                                        ⟵|
```

Fig. 39. DNA sequence of coding region in pmTTk
(Upper: Coding chain
Lower: Coded amino acid sequence)

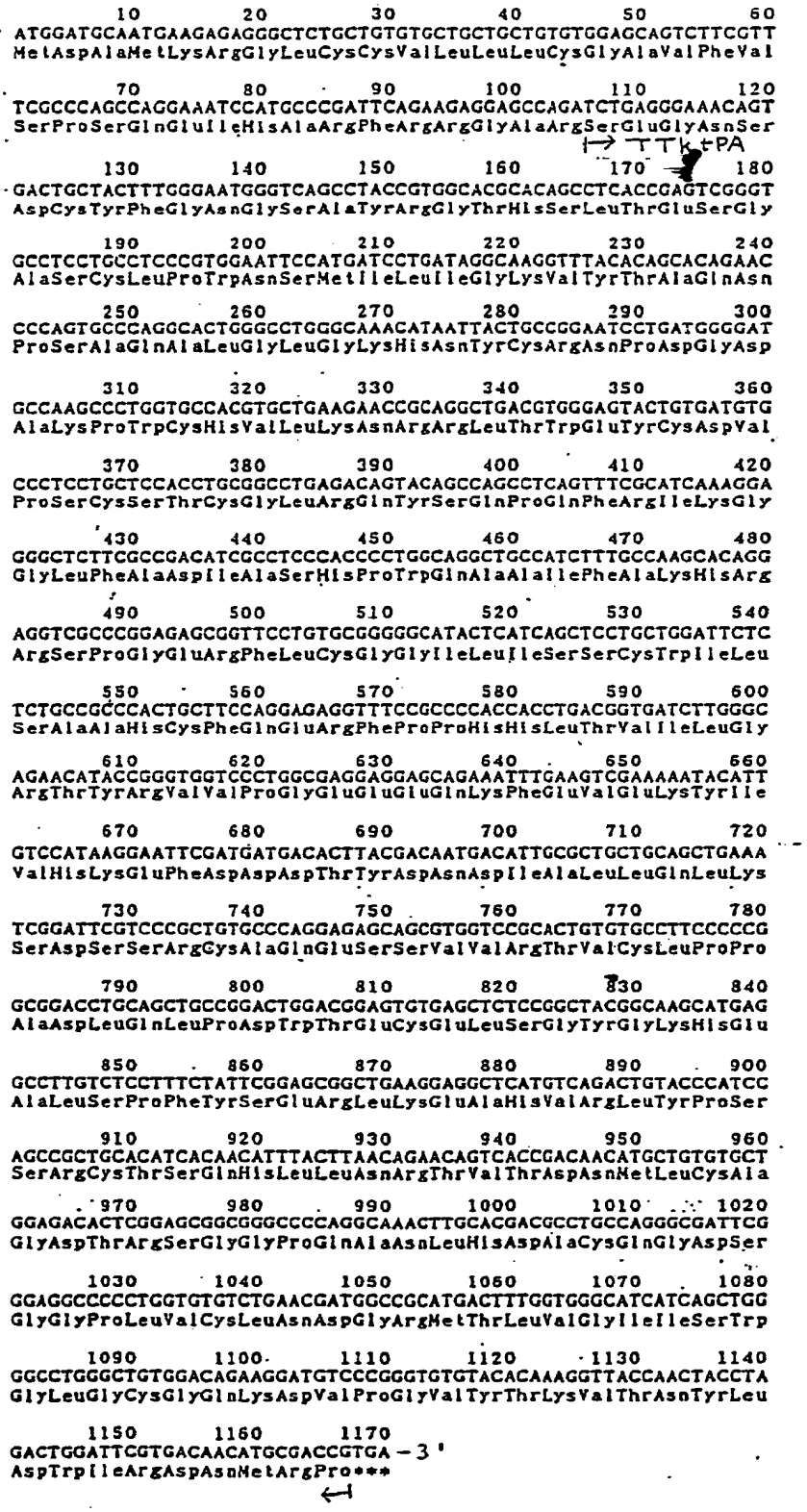


Fig. 40. DNA sequence of coding region in pmSTTk
(Upper: Coding chain
Lower: Coded amino acid sequence)

```
                10          20          30          40          50          60
5'- ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTT
    MetAspAlaMetLysArgGlyLeuCysCysValLeuLeuLeuCysGlyAlaValPheVal

               70          80          90         100         110         120
    TCGCCCAGCCAGGAAATCCATGCCCGATTCAGAAGAGGAGCCAGATCTGAGGGAAACAGT
    SerProSerGlnGluIleHisAlaArgPheArgArgGlyAlaArgSerGluGlyAsnSer
                                                  ↦ STTkとPA
              130         140         150         160         170         180
    GACTGCTACTTTGGGAATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCGGGT
    AspCysTyrPheGlyAsnGlySerAlaTyrArgGlyThrHisSerLeuThrGluSerGly

              190         200         210         220         230         240
    GCCTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTTTACACAGCACAGAAC
    AlaSerCysLeuProTrpAsnSerMetIleLeuIleGlyLysValTyrThrAlaGlnAsn

              250         260         270         280         290         300
    CCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATTACTGCCGGAATCCTGATGGGGAT
    ProSerAlaGlnAlaLeuGlyLeuGlyLysHisAsnTyrCysArgAsnProAspGlyAsp

              310         320         330         340         350         360
    GCCAAGCCCTGGTGCCACGTGCTGAAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTG
    AlaLysProTrpCysHisValLeuLysAsnArgArgLeuThrTrpGluTyrCysAspVal

              370         380         390         400         410         420
    CCCTCCTGCTCCACCTGCGGCCTGAGACAGTACAGCCAGCCACAGTTTGATATCAAAGGA
    ProSerCysSerThrCysGlyLeuArgGlnTyrSerGlnProGlnPheAspIleLysGly

              430         440         450         460         470         480
    GGCCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCTTTGCCAAGCACAGG
    GlyLeuPheAlaAspIleAlaSerHisProTrpGlnAlaAlaIlePheAlaLysHisArg

              490         500         510         520         530         540
    AGGTCGCCCGGAGAGCGGTTCCTGTGCGGGGGCATACTCATCAGCTCCTGCTGGATTCTC
    ArgSerProGlyGluArgPheLeuCysGlyGlyIleLeuIleSerSerCysTrpIleLeu

              550         560         570         580         590         600
    TCTGCCGCCCACTGCTTCCAGGAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGC
    SerAlaAlaHisCysPheGlnGluArgPheProProHisHisLeuThrValIleLeuGly

              610         620         630         640         650         660
    AGAACATACCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAATACATT
    ArgThrTyrArgValValProGlyGluGluGluGlnLysPheGluValGluLysTyrIle

              670         680         690         700         710         720
    GTCCATAAGGAATTCGATGATGACACTTACGACAATGACATTGCGCTGCTGCAGCTGAAA
    ValHisLysGluPheAspAspAspThrTyrAspAsnAspIleAlaLeuLeuGlnLeuLys

              730         740         750         760         770         780
    TCGGATTCGTCCCGCTGTGCCCAGGAGAGCAGCGTGGTCCGCACTGTGTGCCTTCCCCCG
    SerAspSerSerArgCysAlaGlnGluSerSerValValArgThrValCysLeuProPro

              790         800         810         820         830         840
    GCGGACCTGCAGCTGCCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAG
    AlaAspLeuGlnLeuProAspTrpThrGluCysGluLeuSerGlyTyrGlyLysHisGlu

              850         860         870         880         890         900
    GCCTTGTCTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACTGTACCCATCC
    AlaLeuSerProPheTyrSerGluArgLeuLysGluAlaHisValArgLeuTyrProSer

              910         920         930         940         950         960
    AGCCGCTGCACATCACAACATTTACTTAACAGAACAGTCACCGACAACATGCTGTGTGCT
    SerArgCysThrSerGlnHisLeuLeuAsnArgThrValThrAspAsnMetLeuCysAla

              970         980         990        1000        1010        1020
    GGAGACACTCGGAGCGGCGGGCCCCAGGCAAACTTGCACGACGCCTGCCAGGGCGATTCG
    GlyAspThrArgSerGlyGlyProGlnAlaAsnLeuHisAspAlaCysGlnGlyAspSer

             1030        1040        1050        1060        1070        1080
    GGAGGCCCCCTGGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCTGG
    GlyGlyProLeuValCysLeuAsnAspGlyArgMetThrLeuValGlyIleIleSerTrp

             1090        1100        1110        1120        1130        1140
    GGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACAAAGGTTACCAACTACCTA
    GlyLeuGlyCysGlyGlnLysAspValProGlyValTyrThrLysValThrAsnTyrLeu

             1150        1160        1170
    GACTGGATTCGTGACAACATGCGACCGTGA-3'
    AspTrpIleArgAspAsnMetArgPro***
                                ↤
```

European Patent Office

EUROPEAN SEARCH REPORT

Application number

DOCUMENTS CONSIDERED TO BE RELEVANT

EP 88112569.4

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int. Cl.4)
X	EP - A2 - 0 199 574 (GENENTECH, INC.) * Fig. 2B-2E; claims 1-4,7-9, 13-20 * --	1-9	C 12 N 15/00 C 07 K 13/00 C 12 N 9/50 C 07 H 21/04 A 61 K 37/54
X	EP - A1 - 0 093 619 (GENENTECH, INC.) * Fig. 5; claims 1-7,9,11-15 * --	1-9	
D,X	EP - A2 - 0 196 920 (BEECHAM GROUP PLC) * Claims 1,8,10,11 * --	1-9, 12,13	
P,X	EP - A1 - 0 241 208 (BEECHAM GROUP PLC) * Claims 1-10,13-15,24 * --	1-9, 12,13	TECHNICAL FIELDS SEARCHED (Int. Cl.4)
P,X	EP - A2 - 0 233 013 (BEECHAM GROUP PLC) * Claims 1-3,7,8,12 * --	1-9, 13,14	C 12 N C 07 K C 07 H A 61 K
X	EP - A2 - 0 201 153 (BEECHAM GROUP PLC) * Claims 1-7,11,14 * ----	1-9	

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
VIENNA	11-11-1988	WOLF

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
Y : particularly relevant if combined with another document of the same category
A : technological background
O : non-written disclosure
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E : earlier patent document, but published on, or after the filing date
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L : document cited for other reasons

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